



## Exhibit A (Page 1 of 14)

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	E	MATE (	ANCEI	0142_NC	r.api		
OIPE	(FF			Fn			Section 1
	(1)	RADEM	¥. 10	2		30	40 52
1 2 1 2001 SED ID NO:3			SGLILSCI				LESVTYLPEKGLYC
APR SO ID NO:4	(1)					MST	LESVTYLPEKGLYC
A COLO NO:5	(1)						
TRADEMAN SEQ ID NO:6							
SEQ ID NO:7				·			
SEQ ID NO:8	(1)			·			MSKPGKPTLNHGLV
SEQ ID NO:9	(1)						
SEQ ID NO:10							
Consensus	(1)						
						·····	Section 2
	(53)		,60	70	80		
							KLDHGSEVRSFSLG
SEQ ID NO:4	(18)	QRLPSS	GRTHGGTE	SLKGKNT	ENMGFYGT	LKMIFYKMKR	KLDHGSEVRSFSLG
SEQ ID NO:5							KLDHGSEVRSFSLG
SEQ ID NO:6						~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	KLDHGSEVRSFSLG
SEQ ID NO:7	(1)					MKR	KLDHGSEVRSFSLG
SEQ ID NO:8	(15)	PVDLKS	SAKEPLPH	QTVMKIF	SISIIAQG	PFCRRRMKR	KLDHGSEVRSFSLG
SEQ ID NO:9				MKIF			KLDHGSEVRSFSLG
SEQ ID NO:10 Consensus				к			KLDHGSEVRSFSLG
Consensus	(55)			r	L	L MIFIKMAR	KLDHGSEVRSFSLG Section 3
	(105)	105 1	10	,120	.130	.140	Section 3
	(105) (105)	KKDCKI					RRITSVQPPTGLQE
SEQ ID NO:4	(70)	KKPCKV	/SEIISII /SEVTSTT	GLVPCSA	TETTEGDLI	AANGQGQQA	RRITSVQPPTGLQE
SEQ ID NO:5	(31)	KKPCKV	/SEYTSTT	GLVPCSA	TPTTFGDLI	RAANGOGOOR	RRITSVQPPTGLQE
SEQ ID NO:6	(23)	KKPCKV	SEYTSTT	GLVPCSA	TPTTFGDLI	RAANGOGOOR	RRITSVQPPTGLQE
							RRITSVQPPTGLQE
							RRITSVQPPTGLQE
							RRITSVQPPTGLQE
							RRITSVQPPTGLQE
Consensus	(105)	KKPCKV	SEYTSTT	GLVPCSA	TPTTFGDL	RAANGQGQQR	RRITSVQPPTGLQE
							Section 4
	(157)	157		,170	,180	,190	208
SEQ ID NO:3	(157)	WLKMFQ	SWSGPEK	LLALDEL	IDSCEPTQ	KHMMQVIEP	QFQRDFISLLPKEL
SEQ ID NO:4	(122)	WLKMFQ	SWSGPEK	LLALDEL	IDSCEPTQV	/KHMMQVIEP	QFQRDFISLLPKEL
							QFQRDFISLLPKEL
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							QFQRDFISLLPKEL
Consensus	(157)	WLKMFQ	ISWSGPEK	гтагрыг	TDSCEPTO/	VKHMMQVIEP(	QFQRDFISLLPKEL

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(209)209220230240250260SEQ ID NO:3 (209)ALYULSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEEGIDEPLHIKRRKSEQ ID NO:6 (127)ALYULSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEEGIDEPLHIKRRKSEQ ID NO:6 (127)ALYULSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEEGIDEPLHIKRRKSEQ ID NO:6 (127)ALYULSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEEGIDEPLHIKRRKSEQ ID NO:6 (127)ALYULSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEEGIDEPLHIKRRKSEQ ID NO:6 (171)ALYULSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEEGIDEPLHIKRRKSEQ ID NO:8 (171)ALYULSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEEGIDEPLHIKRRKSEQ ID NO:9 (141)ALYULSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEEGIDEPLHIKRRKSEQ ID NO:10 (122)ALYULSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEEGIDEPLHIKRRKConsensus (209)ALYULSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEEGIDEPLHIKRRKConsensus (209)ALYULSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEEGIDEPLHIKRRKSEQ ID NO:10 (122)ALYULSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEEGIDEPLHIKRRKSEQ ID NO:3 (261)VIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGNSEQ ID NO:3 (261)VIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGNSEQ ID NO:6 (177)VIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGNSEQ ID NO:7 (174)VIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGNSEQ ID NO:8 (23)VIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGNSEQ ID NO:8 (23)VIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGNSEQ ID NO:3 (313)RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLKSEQ ID NO:3 (233)RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLKSEQ ID NO:6 (231) </th
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SEQ ID NO:7 (174) VIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGN SEQ ID NO:8 (223) VIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGN SEQ ID NO:9 (193) VIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGN SEQ ID NO:10 (174) VIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGN Consensus (261) VIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGN Section 7 (313) <u>313</u> <u>320</u> <u>330</u> <u>340</u> <u>350</u> <u>364</u> SEQ ID NO:3 (313) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:4 (278) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:5 (239) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:6 (231) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:6 (231) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:7 (226) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:8 (275) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:9 (245) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:9 (245) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:10 (226) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK Consensus (313) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK
SEQ ID NO:8 (223) VIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGN SEQ ID NO:9 (193) VIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGN SEQ ID NO:10 (174) VIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGN Consensus (261) VIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGN (313) <u>313</u> <u>320</u> <u>330</u> <u>340</u> <u>350</u> <u>364</u> SEQ ID NO:3 (313) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:4 (278) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:5 (239) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:6 (231) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:6 (231) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:6 (231) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:6 (251) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:7 (226) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:8 (275) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:9 (245) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:10 (226) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK Consensus (313) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK
SEQ ID NO:9 (193) VIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGN SEQ ID NO:10 (174) VIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGN Consensus (261) VIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGN Section 7 (313) 313 320 330 340 350 364 SEQ ID NO:3 (313) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:4 (278) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:5 (239) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:6 (231) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:6 (231) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:7 (226) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:8 (275) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:9 (245) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:10 (226) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK Consensus (313) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK
SEQ ID NO:10 (174) VIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGN Consensus (261) VIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGN (313) 313 320 330 340 350 Section 7 (313) 313 RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:3 (313) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:4 (278) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:5 (239) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:6 (231) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:6 (231) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:7 (226) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:9 (245) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:9 (245) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:10 (226) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK
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(313)313320330340350364SEQ ID NO:3 (313)RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLKSEQ ID NO:4 (278)RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLKSEQ ID NO:5 (239)RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLKSEQ ID NO:6 (231)RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLKSEQ ID NO:6 (231)RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLKSEQ ID NO:7 (226)RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLKSEQ ID NO:8 (275)RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLKSEQ ID NO:9 (245)RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLKSEQ ID NO:10 (226)RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLKSEQ ID NO:10 (226)RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK
SEQ ID NO:3 (313) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:4 (278) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:5 (239) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:6 (231) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:7 (226) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:8 (275) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:9 (245) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:9 (245) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:10 (226) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIISGSTDRTLK
SEQ ID NO:4 (278) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:5 (239) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:6 (231) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:7 (226) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:8 (275) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:9 (245) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:10 (226) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK
SEQ ID NO:5 (239) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:6 (231) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:7 (226) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:8 (275) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:9 (245) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:10 (226) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:10 (226) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:10 (226) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK Consensus (313) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:10 (226) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIISGSTDRTLK
SEQ ID NO:6 (231) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:7 (226) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:8 (275) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:9 (245) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:10 (226) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK Consensus (313) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK Section 8
SEQ ID NO:7 (226) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:8 (275) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:9 (245) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:10 (226) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK Consensus (313) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK Seq ID NO:10 (226) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK Consensus (313) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIISGSTDRTLK
SEQ ID NO:8 (275) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:9 (245) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:10 (226) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK Consensus (313) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK Section 8
SEQ ID NO:9 (245) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK SEQ ID NO:10 (226) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK Consensus (313) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK Section 8
SEQ ID NO:10 (226) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK Consensus (313) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK Section 8
Consensus (313) RIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK Section 8
Section 8
(365) <u>365</u> <u>370</u> <u>380</u> <u>390</u> <u>400</u> 416
SEQ ID NO:3 (365) VWNAETGECIHTLYGHTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCLHV
SEQ ID NO:4 (330) VWNAETGECIHTLYGHTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCLHV
SEQ ID NO:5 (291) VWNAETGECIHTLYGHTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCLHV
SEQ ID NO:6 (283) VWNAETGECIHTLYGHTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCLHV
SEQ ID NO:7 (278) VWNAETGECIHTLYGHTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCLHV
SEQ ID NO:8 (327) VWNAETGECIHTLYGHTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCLHV
SEQ ID NO:9 (297) VWNAETGECIHTLYGHTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCLHV
SEQ ID NO:10 (278) VWNAETGECIHTLYGHTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCLHV
Consensus (365) VWNAETGECIHTLYGHTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCLHV

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					Section 9
(417	417	,430	,440	450	468
SEQ ID NO:3 (417	LMGHVAAVR	CVQYDGRRVV	SGAYDFMVKV	WDPETETCLHTL	GHTNRVYSLO
SEQ ID NO:4 (382	LMGHVAAVR	CVQYDGRRVV	SGAYDFMVKV	WDPETETCLHTL	GHTNRVYSLQ
				WDPETETCLHTL	
SEQ ID NO:6 (335	LMGHVAAVR	CVQYDGRRVV	SGAYDFMVKV	WDPETETCLHTL	GHTNRVYSLO
SEQ ID NO:7 (330	LMGHVAAVR	CVQYDGRRVV	SGAYDFMVKV	WDPETETCLHTL	GHTNRVYSLQ
				WDPETETCLHTL	
SEQ ID NO:9 (349)	LMGHVAAVR	CVQYDGRRVV	SGAYDFMVKV	WDPETETCLHTL	GHTNRVYSLQ
SEQ ID NO:10 (330)	LMGHVAAVR	CVQYDGRRVV	SGAYDFMVKV	WDPETETCLHTL	GHTNRVYSLQ
Consensus (417)	LMGHVAAVR	CVQYDGRRVV	SGAYDFMVKV	WDPETETCLHTL	GHTNRVYSLQ
					Section 10
(469)	469	480	,490	5005	520
				TGHQSLTSGMEL	
SEQ ID NO:4 (434)	FDGIHVVSG	SLDTSIRVWD	VETGNCIHTL	TGHQSLTSGMELE	CDNILVSGNAD
SEQ ID NO:5 (395)	FDGIHVVSG	SLDTSIRVWD	VETGNCIHTL	TGHQSLTSGMELH	CDNILVSGNAD
SEQ ID NO:6 (387)	FDGIHVVSG	SLDTSIRVWD	VETGNCIHTL	TGHQSLTSGMELH	KDNILVSGNAD
SEQ ID NO:7 (382)	FDGIHVVSG	SLDTSIRVWD	VETGNCIHTL	TGHQSLTSGMELH	CDNILVSGNAD
SEQ ID NO:8 (431)	FDGIHVVSG	SLDTSIRVWD	VETGNCIHTL	TGHQSLTSGMELE	<b>CDNILVSGNAD</b>
SEQ ID NO:9 (401)	FDGIHVVSG	SLDTSIRVWD	VETGNCIHTL	TGHQSLTSGMELH	(DNILVSGNAD
SEQ ID NO:10 (382)	FDGIHVVSG	SLDTSIRVWD	VETGNCIHTL	TGHQSLTSGMELH	CDNILVSGNAD
Consensus (469)	FDGIHVVSG	SLDTSIRVWD	VETGNCIHTL	TGHQSLTSGMELH	K D N I L V S G N A D
······ ·					——– Section 11
(521)				<u>550 560 </u>	572
				LQFNKNFVITSSI	
Consensus (521)	STVKIWDIK	IGQCLQTLQG	PNKHQSAVTC	LQFNKNFVITSSI	
					—— Section 12
		E00	600	C10	624
(573)		590			
SEQ ID NO:3 (573)	TGEFIRNLV	LESGGSGGV	VWRIRASNTK	LVCAVGSRNGTEE	TKLLVLDFDV
SEQ ID NO:3 (573) SEQ ID NO:4 (538)	TGEFIRNLV? TGEFIRNLV?	LESGGSGGV LESGGSGGV	VWRIRASNTK VWRIRASNTK	LVCAVGSRNGTEE LVCAVGSRNGTEE	TKLLVLDFDV TKLLVLDFDV
SEQ ID NO:3 (573) SEQ ID NO:4 (538) SEQ ID NO:5 (499)	TGEFIRNLV TGEFIRNLV TGEFIRNLV	LESGGSGGV LESGGSGGV LESGGSGGV	VWRIRASNTK VWRIRASNTK VWRIRASNTK	LVCAVGSRNGTEE LVCAVGSRNGTEE LVCAVGSRNGTEE	TKLLVLDFDV TKLLVLDFDV TKLLVLDFDV
SEQ ID NO:3 (573) SEQ ID NO:4 (538) SEQ ID NO:5 (499) SEQ ID NO:6 (491)	TGEFIRNLV TGEFIRNLV TGEFIRNLV TGEFIRNLV	LESGGSGGV LESGGSGGV LESGGSGGV LESGGSGGV	VWRIRASNTK VWRIRASNTK VWRIRASNTK VWRIRASNTK	LVCAVGSRNGTEE LVCAVGSRNGTEE LVCAVGSRNGTEE LVCAVGSRNGTEE	TKLLVLDFDV TKLLVLDFDV TKLLVLDFDV TKLLVLDFDV
SEQ ID NO:3 (573) SEQ ID NO:4 (538) SEQ ID NO:5 (499) SEQ ID NO:6 (491) SEQ ID NO:7 (486)	TGEFIRNLV TGEFIRNLV TGEFIRNLV TGEFIRNLV TGEFIRNLV	LESGGSGGV LESGGSGGV LESGGSGGV LESGGSGGV LESGGSGGV	VWRIRASNTK VWRIRASNTK VWRIRASNTK VWRIRASNTK VWRIRASNTK	LVCAVGSRNGTEE LVCAVGSRNGTEE LVCAVGSRNGTEE LVCAVGSRNGTEE LVCAVGSRNGTEE	TKLLVLDFDV TKLLVLDFDV TKLLVLDFDV TKLLVLDFDV TKLLVLDFDV
SEQ ID NO:3 (573) SEQ ID NO:4 (538) SEQ ID NO:5 (499) SEQ ID NO:6 (491) SEQ ID NO:7 (486) SEQ ID NO:8 (535)	TGEFIRNLV TGEFIRNLV TGEFIRNLV TGEFIRNLV TGEFIRNLV TGEFIRNLV	LESGGSGGV LESGGSGGV LESGGSGGV LESGGSGGV LESGGSGGV	VWRIRASNTK VWRIRASNTK VWRIRASNTK VWRIRASNTK VWRIRASNTK VWRIRASNTK	LVCAVGSRNGTEE LVCAVGSRNGTEE LVCAVGSRNGTEE LVCAVGSRNGTEE LVCAVGSRNGTEE LVCAVGSRNGTEE	TKLLVLDFDV TKLLVLDFDV TKLLVLDFDV TKLLVLDFDV TKLLVLDFDV TKLLVLDFDV
SEQ ID NO:3 (573) SEQ ID NO:4 (538) SEQ ID NO:5 (499) SEQ ID NO:6 (491) SEQ ID NO:7 (486) SEQ ID NO:8 (535) SEQ ID NO:9 (505)	TGEFIRNLV TGEFIRNLV TGEFIRNLV TGEFIRNLV TGEFIRNLV TGEFIRNLV	LESGGSGGV LESGGSGGV LESGGSGGV LESGGSGGV LESGGSGGV LESGGSGGV	VWRIRASNTK VWRIRASNTK VWRIRASNTK VWRIRASNTK VWRIRASNTK VWRIRASNTK VWRIRASNTK	LVCAVGSRNGTEE LVCAVGSRNGTEE LVCAVGSRNGTEE LVCAVGSRNGTEE LVCAVGSRNGTEE LVCAVGSRNGTEE LVCAVGSRNGTEE	TKLLVLDFDV TKLLVLDFDV TKLLVLDFDV TKLLVLDFDV TKLLVLDFDV TKLLVLDFDV TKLLVLDFDV
SEQ ID NO:3 (573) SEQ ID NO:4 (538) SEQ ID NO:5 (499) SEQ ID NO:6 (491) SEQ ID NO:7 (486) SEQ ID NO:8 (535) SEQ ID NO:9 (505) SEQ ID NO:10 (486)	TGEFIRNLV TGEFIRNLV TGEFIRNLV TGEFIRNLV TGEFIRNLV TGEFIRNLV TGEFIRNLV	LESGGSGGV LESGGSGGV LESGGSGGV LESGGSGGV LESGGSGGV LESGGSGGV LESGGSGGV	VWRIRASNTK VWRIRASNTK VWRIRASNTK VWRIRASNTK VWRIRASNTK VWRIRASNTK VWRIRASNTK	LVCAVGSRNGTEE LVCAVGSRNGTEE LVCAVGSRNGTEE LVCAVGSRNGTEE LVCAVGSRNGTEE LVCAVGSRNGTEE	TKLLVLDFDV TKLLVLDFDV TKLLVLDFDV TKLLVLDFDV TKLLVLDFDV TKLLVLDFDV TKLLVLDFDV TKLLVLDFDV

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- Section 13

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(625) 6227 SEQ ID NO:3 (625) DMK SEQ ID NO:4 (590) DMK SEQ ID NO:5 (551) DMK SEQ ID NO:6 (543) DMK SEQ ID NO:7 (538) DMK SEQ ID NO:9 (557) DMK SEQ ID NO:10 (538) DMK SEQ ID NO:10 (538) DMK

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(1)         10         20         30         40         52           SEQ ID NO:1         (1)																									Sect	ion 1
$\begin{array}{cccc} {\rm SEQ} \mbox{ID}\ NO:2 & (1) \mbox{C} C \mbox{C} a \mbox{G} C \mbox{G} C \mbox{G} C \mbox{G} C \mbox{I} \\ (1) \mbox{C} \mbox{A} \mbox{T} \mbox{T} \mbox{G} \mbox{G}$																										
$\begin{array}{cccc} {\rm SEQ} \mbox{ID}\ NO:2 & (1) \mbox{C} C \mbox{C} a \mbox{G} C \mbox{G} C \mbox{G} C \mbox{G} C \mbox{I} \\ (1) \mbox{C} \mbox{A} \mbox{T} \mbox{T} \mbox{G} \mbox{G}$	SEQ ID NO:1	(1)						СТС	ΑT	TA	TT	СС	CT	CG.	AGT	TC		·TT	CI	'CA	GТ	CA	A-	6	CTO	CAT
Section 2         Section 2           SEQ ID NO:1         (39) GTATGTATGTGGTCCCGAGAAGCGGTTTGATACTGAGCTGCATTTGCC- SEQ ID NO:2         (53) GCTT-GGTTCTCAGCCTTTTAAAAACTATTATTATATATATTTTTAAAA Consensus         (53) G T G T T G C AA TT TA A T TTT           Consensus         (53) G T G T T G C AA TT TA A T TTT         TA A T TTT           (105) 105         110         ,120         ,130         140           SEQ ID NO:1         (88) TTTACTGTGGAG-TTTTGTTGCCGGTTCTGC-TCCCTAATCTTCCTTTTC SEQ ID NO:2         (105) TTTATGTGGTTAGAGCTTTTAGTATGTGCCGTGTATTACATGTAGAGAGTATT Consensus         105) TTTA TG T GAG TTTT T G CTG T C T T T           (105) 157         170         ,180         190         208           SEQ ID NO:1         (136) TGACGTGCCTGAGCA-TGTCCACAT-TAGAAACTGGGACA-AAACCTACCTAA         Section 5         Section 5           SEQ ID NO:1         136         TGCAACCAAGAGGAGTTTTAAAAAGTCCAAAACCGGGACA-AAACCTACCTAA         Consensus         (157) G C C GAG A T T A AT T AA C G G A A ACCTACC TA A           SEQ ID NO:2         (157) G C C C GAG A T T A AT T AA C G GA A ACCTACC CTA A         Section 5         Section 5           (209) 209         220         230         240         250         260           SEQ ID NO:2         (180) AAAGGTTACTGGAGAGTGCCAAAGCAGCGGACAACACGGGCCACAC         Section 5         Section 5         Section 5           (209) 209         209         230         <	SEQ ID NO:2	(1)	СТ	CA	GC	AG	GT	CAG	GA	CA	TT	ΤG	GT	AG	GGG	AA	GG	TT	GA	AA	GA	CA	AA	AG	CAC	GCAG
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	Consensus	(1)						С		Α	ТΤ		Т	G	G		-	TT		Α	G	CA	Α	G	ic (	SCA
SEQ ID NO:1(39) GTAT GTATGTGTGTCCCGAGAAGCGGTTTGATACTGAGCTGCATTTGCC-SEQ ID NO:2(53) G C T G T T G C AA TT TA A T TTTConsensus(53) G T G T T G C AA TT TA A T TTTConsensus(53) G T G T T G C AA TT TA A T TTT(105)105110(105)105110(105)TTTACTGTGGAG-TTTTGTGCCGGTTCTGC-TCCCTAATCTTCCTTTTCSEQ ID NO:1(88)(105)TTTA TG T GAG TTTT T G CTG T C T T TConsensus(105)(105)TTTA TG T GAG TTTT T G CTG T C T T TConsensus(105)(105)157(105)110(105)157(105)157(105)157(105)157(105)157(105)157(105)157(105)162(209)20920020025026026026026026026																									<ul> <li>Sect</li> </ul>	ion 2
SEQ ID NO:2       (53)       GCCTTGGGTTCTCAGCCTTTTAAAAACTATTATTAAATATATAT																	_									
Consensus         (53)         G         T         G         T         T         G         C         AA         TT         TA         A         T         TTT         Section 3         Section 3           SEQ ID NO:1         (105)         105         ,110         ,120         ,130         ,140         156           SEQ ID NO:2         (105)         TTTAGTGGTTAGAGCTTTTGGTGCCTGTATTACATGTAGAGAGTATT         G         CTG         T         C         T <td< td=""><td>SEQ ID NO:1</td><td>(39)</td><td>GT</td><td>ΑT</td><td></td><td>GΤ</td><td>AT</td><td>GTG</td><td>ΤG</td><td>TC</td><td>CC</td><td>GA</td><td>GA</td><td>AG</td><td>CGG</td><td>ΤТ</td><td>ΤC</td><td>AT</td><td>AC</td><td>TG</td><td>AG</td><td>СТ</td><td>GC</td><td>AT</td><td>TTC</td><td>GCC-</td></td<>	SEQ ID NO:1	(39)	GT	ΑT		GΤ	AT	GTG	ΤG	TC	CC	GA	GA	AG	CGG	ΤТ	ΤC	AT	AC	TG	AG	СТ	GC	AT	TTC	GCC-
Section 3           (105)         105         110         120         130         140         156           SEQ ID NO:1         (88)         TTTACTG - TGGAG - TTTTGGTGCCGGTCTGC - TCCCTAATCTTCCTTTTC GONSENSUS (105)         TTTAGT GGTTAGAGCTTTTAGTAATGTGCCGGTATTACATGTAGAGAGTATT CONSENSUS (105)         TTTA TG         T         G         CTG         T         T         T           Consensus (105)         TTTA TG         T         GAG         TTTT         T         G         CTG         T         T         T           SEQ ID NO:1         (136)         TGACGTGCCTGAGCA - TGTCCACAT - TAGAATCTGTGGACATACCTAC - CTGA         Section 4         Section 4         Section 4         Section 4         Section 5         Section 6         Section 5         Section 6         Section 7         Section 7         Section 7         Section 7 </td <td>SEQ ID NO:2</td> <td>(53)</td> <td>GC</td> <td>СТ</td> <td>ΤG</td> <td>GG</td> <td>ТТ</td> <td>CTC</td> <td>AG</td> <td>CC</td> <td>ΤT</td> <td>ΤТ</td> <td>AA</td> <td>AA.</td> <td>АСТ</td> <td>ΑT</td> <td>ΤA</td> <td>TT</td> <td>AA</td> <td>AT</td> <td>ΑT</td> <td>AT</td> <td>ΤA</td> <td>TT</td> <td>TTZ</td> <td>AAA</td>	SEQ ID NO:2	(53)	GC	СТ	ΤG	GG	ТТ	CTC	AG	CC	ΤT	ΤТ	AA	AA.	АСТ	ΑT	ΤA	TT	AA	AT	ΑT	AT	ΤA	TT	TTZ	AAA
(105)       105       110       120       130       140       156         SEQ ID NO:2       (105)       TTACTG - TGGAG - TTTTGTTGCCGGTTCTGC - TCCCTAATCTTCCTTTC       SEQ ID NO:2       (105)       TTAG G GTTAGAGCTTTTAGTAATGTGCCTGTATTACATGTAGAGAGTATT         Consensus       (105)       TTAG G GTTAGAGCTTTTAGTAATGTGCCGGTCTGACATCTTCCTTTC       Section 4       T	Consensus	(53)	G	Т		G	Т	Т	G	С			A	A		Т	т	Т	Α		A	Т		Т	ΤT	
SEQ ID NO:1       (88)       TTTACTG - TGGAG - TTTTGTTGCCGGTTCTGC - TCCCTAATCTTCCTTTTC         SEQ ID NO:2       (105)       TTTAGTGGTTAGAGCTTTTAGTAATGTGCCTGTATTACATGTAGAGAGTATT         Consensus       (105)       TTTA TG       T       GAG       TTT       T       G       CTG       T       C       T       T       T         Consensus       (105)       TTTA TG       T       GAG       TTT       T       G       CTG       T       C       T       T       T       T       Section 4         (157)       157       .170       .180       .190       208       Section 4         (157)       CGTCAACCAAGAGGAGTTTTAAAATGTCAAAACCGGGAAAAACCTACTACCACAC       CTG       A       ACCTAC       CTA         SEQ ID NO:2       (157)       CGC       C       GAG       A       T       A       AT       T       AA       C       G       GA       ACCTAC       CT       Section 5       Section 6       Section 6       Section 6 <td></td> <td>Sect</td> <td>ion 3</td>																									Sect	ion 3
SEQ ID NO:2       (105)       TTTAGTGGTTAGAGCTTTTAGTAATGTGCCTGTATTACATGTAGAGAGATATT         Consensus       (105)       TTTA <tg< td="">       T       GAG       TTT       T       G       CTG       T       C       T&lt;</tg<>		(105)	105		_1	10				, <mark>12</mark> 0	)				130				_1	40						156
Consensus       (105)       TTTA TG       T       GAG       CTG       T       C       T       T       T       Section 4         (157)       157       170       180       190       208         SEQ ID NO:1       1136       TGACGTGCCTGAGCA-TGTCCACAT-TAGAATCTGTGACATACCTAC-CTGA         SEQ ID NO:2       157)       G C       C       GAG A T       T       A AT       T       AA       ACCTAC       CT       Section 5         SEQ ID NO:1       (185)       AAAAGGTTATATATGCCAGAGACTGCCAAGCAGGGGACACAGGGGGGCACA       Section 5       Section 5       Section 5         (209)       209       220       230       240       250       260         SEQ ID NO:1       (185)       AAAAGGTTTATATGTCAGAGACTGCCAAGCCGGACACACGGGGGGCACA       Section 5       Section 5         (209)       209       220       230       240       250       260         SEQ ID NO:1       (185)       AAAAGGTTTATATGTCAGAGACTGCCAAGCCGGACACACGGGGGCACA       Section 6       Section 6       261       261       270       280       290       300       312         SEQ ID NO:1       (237)       G-AATCACGGAGAGGGGAAAAATACGAAAAATATGGGTTCTACGGCACATTA       Section 6       Section 7       Section 7         (211) <td>SEQ ID NO:1</td> <td>(88)</td> <td>TT</td> <td>ΤA</td> <td>CT</td> <td>G -</td> <td>- T</td> <td>GGA</td> <td>G -</td> <td>ΤT</td> <td>T T</td> <td>GΤ</td> <td>TG</td> <td>CC</td> <td>GGT</td> <td>ТC</td> <td>ΤG</td> <td>- C</td> <td>TC</td> <td>CC</td> <td>ТΑ</td> <td>AT</td> <td>CI</td> <td>TC</td> <td>CTT</td> <td>TTC</td>	SEQ ID NO:1	(88)	TT	ΤA	CT	G -	- T	GGA	G -	ΤT	T T	GΤ	TG	CC	GGT	ТC	ΤG	- C	TC	CC	ТΑ	AT	CI	TC	CTT	TTC
Section 4       Section 4         (157)       157       170       180       190       208         SEQ ID NO:1       (136)       TGACGTGCCTGAGCA-TGTCCACAT-TAGAATCTGTGACATACCTAC-CTGA         SEQ ID NO:2       (157)       G C C G CAACCAAGAGGGAGTTTAAAAATGTCAAAACCGGGA-AAACCTACTCTAA         Consensus       (157)       G C C G GA A T T A AT A C G GA A ACCTAC CT A         Consensus       (157)       G C C G GA A T T A AT A C G GA A ACCTAC CT A         SEQ ID NO:1       (185)       AAAAGGTTTATATTGTCAGAGACTGCCAAGCAGCCGGACACACGGGGGCACA         SEQ ID NO:1       (185)       AAAAGGCTTGGTTCCTGTTGATCTTAAAAGTGCAAAAGAGCCTCTACCACA         SEQ ID NO:2       (208)       ACCATGGCTTGGTTCCTGTTGATCTTAAAAGTGCAAAAGAGCCTCTACCACA         Consensus       (209)       A G T TT GA AA GC A A C CACA         SEQ ID NO:1       (237)       G-AATCACTGAAGGGGAAAAATACAGAAAATATGGGTTTCTACGGCACATTA         SEQ ID NO:1       (261)       261       270       280       290       300       312         SEQ ID NO:2       (260)       TCAAACCGTGATGAAGATATTAGCATTAGCATCACTGGGCACATGGC TCC       Section 7       Section 7         SEQ ID NO:1       (231)       313       320       330       340       350       364         SEQ ID NO:1       (288)       AAATGATTTTTACAAAAGAAAGAAAGAAAGTTGGACCATGGTC	SEQ ID NO:2	(105)	TT	ТΑ	GT	GG	ТT	AGA	GC	ΤT	ŤΤ	AG	TAZ	AT	GT G	C <b>C</b>	ТG	;TA	TΤ	AC	ΑТ	GΤ	AG	AG	AGI	ATT
(157)       157       170       180       190       208         SEQ ID NO:1       (136)       TGACGTGCCTGAGCA-TGTCCACAT-TAGAATCTGTGACATACCTAC-CTGA         SEQ ID NO:2       (157)       CGTCAACCAAGAGGGAGTTTTAAAATGTCAAAACCGGGA-AAACCTACTCTAA         Consensus       (157)       G       C       GAG       A       T       A       AT       T       AA       C       G       GA       A       ACCTAC       CT       A         Consensus       (157)       G       C       C       GAG       A       T       A       AT       T       AA       C       G       GA       A ACCTAC       CT       A         Consensus       (157)       G       C       C       GAG       A       T       A       AT       T       AA       C       G       GA       A ACCTAC       CT       A         Consensus       (10)       NO:2       (208)       ACCATGGCTTGGTTCCTGTGGTCCTAGAGACGCGAAAAAGGCCCACACACA	Consensus	(105)	ΤT	ТΑ	. Т	G	Т	GA	G	ΤТ	ТΤ		т		G	С	ΤG	;	т	С		Т			3	Т
SEQ ID NO:1       (136)       TGACGTGCCTGAGCA-TGTCCACAT-TAGAATCTGTGACATACCTAC-CTGA         SEQ ID NO:2       (157)       CGTCAACCAAGAGGGGGTTTTAAAATGTCAAAACCGGGA-AAACCTACTCTAA         Consensus       (157)       G       C       C       GAG       A       T       A       AT       T       AA       C       G       GA       A       ACCTAC       CT       A         Consensus       (157)       G       C       C       GAG       A       T       T       A       AT       T       AA       C       G       GA       A       ACCTAC       CT       A         Consensus       (157)       G       C       C       GAG       A       T       T       A       AT       T       A       ACCTAC       CT       A         SEQ ID NO:1       (185)       AAAAGGTTTATATATGTGTCAGAGACTGCCAAGCGGGACAACACGGGGCCCCACACAC       Section 5       Section 5       Section 6       C       C       CACA         Consensus       (209)       A       G       T       T       GA       A       C       CACA         SEQ ID NO:1       (237)       G-AATCACTGGAAGAGATATTTAGCATTAGCATCATTGCCCAAGGCCCACATGG       Section 7       Section 7       Section 7       Section 7																									Sect	ion 4
SEQ ID NO:1       (136)       TGACGTGCCTGAGCA-TGTCCACAT-TAGAATCTGTGACATACCTAC-CTGA         SEQ ID NO:2       (157)       CGTCAACCAAGAGGGGGTTTTAAAATGTCAAAACCGGGA-AAACCTACTCTAA         Consensus       (157)       G       C       C       GAG       A       T       A       AT       T       AA       C       G       GA       A       ACCTAC       CT       A         Consensus       (157)       G       C       C       GAG       A       T       T       A       AT       T       AA       C       G       GA       A       ACCTAC       CT       A         Consensus       (157)       G       C       C       GAG       A       T       T       A       AT       T       A       ACCTAC       CT       A         SEQ ID NO:1       (185)       AAAAGGTTTATATATGTGTCAGAGACTGCCAAGCGGGACAACACGGGGCCCCACACAC       Section 5       Section 5       Section 6       C       C       CACA         Consensus       (209)       A       G       T       T       GA       A       C       CACA         SEQ ID NO:1       (237)       G-AATCACTGGAAGAGATATTTAGCATTAGCATCATTGCCCAAGGCCCACATGG       Section 7       Section 7       Section 7       Section 7										)		_	Ĵ	180				1								
SEQ ID NO:2       (157) CGTCAACCAAGAGAGAGTTTTAAAATGTCAAAACCGGGA-AAACCTACTCTAA         Consensus       (157) G C C GAG A T T A AT T AA C G GA A ACCTAC CT A         Section 5         (209)       209       220       230       240       250       260         Section 5         Section 6         Section 6         Colspan="2">Section 6         Section 6         Section 6         Section 6         Section 6         Section 6         Section 7	SEQ ID NO:1	(136)	TG.	AC	GT	GC	СТ	GAG	CA	-T	GT	CC.	ACI	AT	-TA	GA	AT	СТ	GT	GA	CA	ТΑ	.cc	TA	C-C	TGA
Section 5(209)209220230240250260SEQ ID NO:1(185)AAAAGGTTTATATTGTCAGAGACTGCCAAGCAGCCGGACACACGGGGGCACASEQ ID NO:2(208)A C C A G C T TTGA AA GC A A CCACAConsensus(209)A A G T TTGA AA GC A A CCACA(209)A A G T TTGA AA GC A A CCACASEQ ID NO:1(237)G-AATCACTGAAGGGGAAAAATACAGAAAATATGGGTTTCTACGGCACATTASEQ ID NO:1(237)G-AATCACTGAAGGGGGAAAAATACAGAAAATAGCATCATTGCCCAAGGC - CTCCConsensus(261)AA CTGA GGA A TA A ATSEQ ID NO:2(260)TCAAACCGTGATGAAGATATTTAGCATTAGCATCATTGCCCAAGGC - CTCCConsensus(261)AA CTGA GGA A TA A ATSEQ ID NO:2(210)CTTTTTGTCGAAGACGGA-TGAAAAGAAAGTTGGACCATGGTTCTGAGGTCCSEQ ID NO:1(288)AAAATGATTTTTTACAAAATGAAAAGAAAGTTGGACCATGGTTCTGAGGTCCSEQ ID NO:2(313)TTACA TGAAAAGAAAGTTGGACCATGGTTCTGAGGTCCSEQ ID NO:1(340)GCTCTTTTTTTTTTTTTTTTTTTTTTTTGGGAAAGAAAGTTGGAACCATGGATCTGAGGTCCSection 8(365)365370380390400SEQ ID NO:1(340)GCTCTTTTTTTTTTTTTTTTTTTTTTTTGGGAAAGAAACCATGCAAAGTCTCAGAATATACAAGTACSEQ ID NO:2(361)GCTCTTTTTTTTTTTTTTTTTTTGGGAAAGAAACCATGCAAAGTCTCAGAATATACAAGTACSEQ ID NO:2(361)GCTCTTTTTTTTTTTTTTTTTTTTTTTGGGAAAGAAACCATGCAAAGTCTCAGAATATACAAGTAC	SEQ ID NO:2	(157)	CG	тС	AA	сc	AA	GAG	GA	GT	TT	TA	AAZ	AT	GTC	AA.	AA	CC	GG	GA	- A	AA	cc	TA	СТС	TAA
(209)       209       220       230       240       250       260         SEQ ID NO:1       (185)       AAAAGGTTTATATTGTCAGAGACTGCCAAGCAGCCGGACACGGGGGCACA         SEQ ID NO:2       (208)       A C C TGGGTTCCTGTTGATCTTAAAAGTGCAAAAGAGCCTCTACCACA         Consensus       (209)       A A G T TT GA AA GC A A C CACA         SEQ ID NO:1       (261)       261       270       280       290       300       312         SEQ ID NO:1       (237)       G-AATCACTGAAGGGGGAAAAATACAGAAAATATGGGTTTCTACGGCACATTA       Section 6       261       261       270       280       290       300       312         SEQ ID NO:1       (237)       G-AATCACTGAAGGGGGAAAAATACAGAAAATATGGGTTTCTACGGCACATTA       SEQ ID NO:2       260)       TCAAACCGTGATGAAGATATTTAGCATTAGCATCATTGCCCAAGGCCTCC         Consensus       (261)       AA C       TGA G       GA A TA       A AT       T       C A GGC       T         (261)       AA C       TGA G       GA A TA       A AT       T       C A GGC       T         SEQ ID NO:2       (261)       AA C       TGA G       GA A TA       A AT       T       C A GGC       T         SEQ ID NO:1       (288)       AAAATGATTTTTTACAAAAGAAAGATGGAACCATGGACCATGGTTCTGAGGTCC       Section 7       Section 8	Consensus	(157)	G	С		С		GAG	Α	Т	Т		A Z	ΑT	т	A	Α	С	G	GA	A	A	CC	TA	.c c	T A
SEQ ID NO:1       (185)       AAAAGGTTTATATTGTCAGAGACTGCCAAGCAGCCGGACACACGGGGGCACA         SEQ ID NO:2       (208)       ACCATGGCTTGGTTCCTGTTGATCTTAAAAGTGCAAAAGAGCCTCTACCACA         Consensus       (209)       A       A       G       T       TT       GA       AA       GC       A       A       C       CACA         Consensus       (209)       A       A       G       T       TT       GA       AA       GC       A       A       C       CACA         SEQ ID NO:1       (237)       G-AATCACTGAAGGGGAAAAATACAGAAAATATGGGTTTCTACGGCACATTA       Section 6       (261)       261       270       280       290       300       312         SEQ ID NO:2       (260)       TCAAACCGTGATGAAGATATTAGCATTAGCATCATTGCCCCAAGGCCTCC       Consensus       (261)       AA       C       TGC       TGC       A       GC       T       Section 7         SEQ ID NO:2       (261)       AA       C       TGA       GA       TA       A       AT       T       C       A GC       TC         SEQ ID NO:1       (288)       AAAATGATTTTTTACAAAATGAAAAGAAAGAAAGTTGGACCATGGTCTGAGGTCC       Section 7       S133       313       320       330       340       350       364         SEQ ID		-																							Sect	ion 5
SEQ ID NO:2       (208) ACCATGGCTTGGTTCCTGTTGATCTTAAAAGTGCAAAAGAGCCTCTACCACA         Consensus       (209) A       A       G       T       TT       GA       AA       GC       A       A       C       CACA         Seq ID NO:1       (261)       261       270       280       290       300       312         SEQ ID NO:1       (237)       G-AATCACTGAAGGGGAAAAATACAGAAAATATGGGTTTCTACGGCACATTA       SEQ ID NO:2       (260)       TCAAACCGTGATGAAGATATTAGCATTAGCATCATTGCCCAAGGCCTCC         Consensus       (261)       AA       C       TGA       G       A       T       C       A GC       T         SEQ ID NO:2       (260)       TCAAACCGTGATGAAGAGATATTAGCATTAGCATCATTGCCCAAGGCCTCC       Section 7       Section 7       Section 7         (313)       313       320       330       340       350       364         SEQ ID NO:1       (288)       AAAATGATTTTTACAAAATGAAAAGAAAGTTGGACCATGGTTCTGAGGTCC       Section 7         SEQ ID NO:2       (310)       CTTTTTGCGAAGACGGA-TGAAAAGAAAGTTGGACCATGGTTCTGAGGTCC       Section 8         (365)       365       370       380       390       400       416         SEQ ID NO:1       (340)       GCTCTTTTTCTTGGGAAAGAAACCATGCAAGGCAAAGTCTCAGAAAGTACCAGGAAAGTACCAAGGCAAAGTCTCAGAATATACAAGTAC <td></td> <td>(209)</td> <td>209</td> <td></td> <td></td> <td></td> <td></td> <td>220</td> <td>)</td> <td></td> <td></td> <td></td> <td>230</td> <td></td> <td></td> <td></td> <td>2</td> <td>40</td> <td></td> <td></td> <td></td> <td>2</td> <td>50</td> <td></td> <td></td> <td>260</td>		(209)	209					220	)				230				2	40				2	50			260
Consensus(209) AAGTTGAAAGCAACCACASEQ ID NO:1(261)261270280290300312SEQ ID NO:1(237)G-AATCACTGAAGGGGAAAAATACAGAAAATATGGGTTTCTACGGCACATTASEQ ID NO:2(260)TCAAACCGTGATGAAGATATTTAGCATTAGCATCATTGCCCAAGGCCTCCConsensus(261)AACTGAGATAAATTCAGCTSEQ ID NO:2(261)AACTGAGGATAAATTCAGCTSection 7(313)313320330340350364SEQ ID NO:1(288)AAAATGATTTTTTACAAAATGAAAAGAAAGATGGACCATGGTTCTGAGGTCCSection 8(310)CTTTTTGTCGAAGACGGA-TGAAAAGAAAGTTGGACCATGGTTCTGAGGTCCSection 8(365)365370380390400416SEQ ID NO:1(340)GCTCTTTTTCTTGGGAAAAGAAAGAAAGCCATGCAAAGTCTCAGAATATACAAGTACSEQ ID NO:2(361)GCTCTTTTTCTTTGGGAAAAGAAACCATGCAAAGTCTCAGAATATACAAGTACSEQ ID NO:2(361)GCTCTTTTTCTTGGGAAAAGAAACCATGCAAAGTCTCAGAATATACAAGTACSEQ ID NO:2(361)GCTCTTTTTCTTGGGAAAGAAACCATGCAAAGTCTCAGAATATACAAGTAC	SEQ ID NO:1	(185)	AA.	AA	GG	ΤТ	ΤA	TAT	ΤG	ТC	AG	AG.	ACT	ΓG	CCA	AG	CA	GC	CG	GA	CA	CA	CC	GGG	GGC	ACA
Section 6(261)261270280290300312SEQ ID NO:1(237)G-AATCACTGAAGGGGAAAAATACAGAAAATATGGGTTTCTACGGCACATTASEQ ID NO:2(260)TCAAACCGTGATGAAGATATTTAGCATTAGCATCATTGCCCAAGGCCTCCConsensus(261)AACTGAGGATAAATTCAGGCTSection 7(313)313320330340350364SEQ ID NO:1(288)AAAATGATTTTTTACAAAATGAAAAGAAAGTTGGACCATGGTTCTGAGGTCCSEQ ID NO:2(310)CTTTTTGTCGAAGACGGA-TGAAAAGAAAGTTGGACCATGGTTCTGAGGTCCSection 8(365)365370380390400416SEQ ID NO:1(340)GCTCTTTTTCTTTGGGAAAGAAAGCATGCAAAGTCTCAGAATATACAAGTACSEQ ID NO:1(340)GCTCTTTTTCTTTGGGAAAGAAACCATGCAAAGTCTCAGAATATACAAGTACSEQ ID NO:2(361)GCTCTTTTTCTTTGGGAAAGAAACCATGCAAAGTCTCAGAATATACAAGTAC	SEQ ID NO:2	(208)	AC	CA	ΤG	GC	ΤТ	GGŢ	ТC	СТ	GT	TG	ATC	СТ	ΓAA	AA	GΤ	GC	AA	AA	GA	GC	СТ	CT	ACC	ACA
(261)261270280290300312SEQ ID NO:1(237)G-AATCACTGAAGGGGAAAAATACAGAAAATATGGGTTTCTACGGCACATTASEQ ID NO:2(260)TCAAACCGTGATGAAGATATTAGCATTAGCATCATTGCCCAAGGCCTCCConsensus(261)AACTGAGGATAAATTCA GGCTSection 7(313)313320330340350364SEQ ID NO:1(288)AAAATGATTTTTTACAAAATGAAAAGAAAGTTGGACCATGGTTCTGAGGTCCSEQ ID NO:2(310)CTTTTTGTCGAAGACGGA-TGAAAAGAAAGTTGGACCATGGTTCTGAGGTCCSEQ ID NO:2(313)TTACATGAAAAGAAAGTTGGACCATGGTTCTGAGGTCCSEQ ID NO:1(340)GCTCTTTTTCTTGGGAAAGAAACCATGCAAAGTCTCAGAATATACAAGTACSEQ ID NO:1(340)GCTCTTTTTCTTGGGAAAGAAACCATGCAAAGTCTCAGAATATACAAGTACSEQ ID NO:2(361)GCTCTTTTTCTTGGGAAAGAAACCATGCAAAGTCTCAGAATATACAAGTACSEQ ID NO:2(361)GCTCTTTTTCTTGGGAAAGAAACCATGCAAAGTCTCAGAATATACAAGTAC	Consensus	(209)	Α	Α	G		Т	Т	т			G.	A		А	A		GC		Α	Α		С		C	ACA
SEQ ID NO:1       (237)       G-AATCACTGAAGGGGAAAAATACAGAAAATATGGGTTTCTACGGCACATTA         SEQ ID NO:2       (260)       TCAAAACCGTGATGAAGATATTTAGCATTAGCATCATTGCCCAAGGCCTCC         Consensus       (261)       AA       C       TGA       G       A       TA       A       AT       T       C       A GGC       T         Section 7         (313)       313       320       330       340       350       364         SEQ ID NO:1         SEQ ID NO:1       (288)       AAAATGATTTTTTACAAAATGAAAAGAAAGTTGGACCATGGTTCTGAGGTCC         SEQ ID NO:2       (310)       CTTTTTGTCGAAGACGGA-TGAAAAGAAAGTTGGACCATGGTTCTGAGGTCC       Section 8         SEQ ID NO:2         (365)       365       370       380       390       400       416         SEQ ID NO:1         SEQ ID NO:1       (365)       365       370       380       390       400       416         SEQ ID NO:1       (340)       GCTCTTTTTCTTTGGGAAAGAAACCATGCAAAGTCTCAGAATATACAAGTAC         SEQ ID NO:1       (361)       GCTCTTTTTCTTTGGGAAAGAAACCATGCAAAGTCTCAGAATATACAAGTAC         SEQ ID NO:2       (361)       GCTCTTTTTCTTTGGGGAAAGAAACCATGCAAAGTCTCAGAATATACAAGTAC <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>-</td> <td></td> <td>-</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>Sect</td> <td>ion 6</td>								-											-						Sect	ion 6
SEQ ID NO:2       (260) TCAAACCGTGATGAAGATATTTAGCATTAGCATCATTGCCCCAAGGCCTCC         Consensus       (261) AA C TGA G GA A TA A AT T C A GGC T         Section 7       (313) 313 320 330 340 350 364         SEQ ID NO:1       (288) AAAATGATTTTTTACAAAATGAAAAGAAAGTTGGACCATGGTTCTGAGGTCC         SEQ ID NO:2       (310) CTTTTTGTCGAAGACGGA-TGAAAAGAAAGTTGGACCATGGTTCTGAGGTCC         SEQ ID NO:2       (313) T T AC A TGAAAAGAAAGTTGGACCATGGTTCTGAGGTCC         SEQ ID NO:1       (365) 365 370 380 390 400 416         SEQ ID NO:1       (340) GCTCTTTTTCTTGGGAAAGAAAGAAAGCATGCAAAGTCTCAGAATATACAAGTAC         SEQ ID NO:2       (361) GCTCTTTTTCTTTGGGAAAGAAACCATGCAAAGTCTCAGAATATACAAGTAC		(261)	261				_27	70			Ĩ	280				29	<del>)</del> 0				_30	00				312
Consensus       (261)       AA       C       TGA       G       GA       TA       A       AT       T       C       A       GGC       T         (313)       313       320       330       340       350       364         SEQ ID NO:1       (288)       AAAATGATTTTTTACAAAATGAAAAGAAAGTTGGACCATGGTTCTGAGGTCC       SEQ ID NO:2       (310)       CTTTTTGTCGAAGACGGA-TGAAAAGAAAGTTGGACCATGGTTCTGAGGTCC       GGGTCC         SEQ ID NO:2       (313)       T       T       AC       A       TGAAAAGAAAGTTGGACCATGGTTCTGAGGTCC         SEQ ID NO:1       (365)       365       370       380       390       400       416         SEQ ID NO:1       (340)       GCTCTTTTTCTTTGGGAAAGAAAGCATGCAAAGTCTCAGAATATACAAGTAC       SEQ ID NO:2       (361)       GCTCTTTTTCTTTGGGAAAGAAACCATGCAAAGTCTCAGAATATACAAGTAC	•																									
Section 7         (313)       313       320       330       340       350       364         SEQ ID NO:1       (288)       AAAATGATTTTTTACAAAATGAAAAGAAAGTTGGACCATGGTTCTGAGGTCC         SEQ ID NO:2       (310)       CTTTTTGTCGAAGACGGA-TGAAAAGAAAGTTGGACCATGGTTCTGAGGTCC         Consensus       (313)       T       T       AC       A       TGAAAAGAAAGTTGGACCATGGTTCTGAGGTCC         SEQ ID NO:1       (365)       365       370       380       390       400       416         SEQ ID NO:1       (340)       GCTCTTTTTCTTTGGGAAAGAAAGAAAGCATGCAAAGTCTCAGAATATACAAGTAC       SEQ ID NO:2       (361)       GCTCTTTTTCTTTGGGAAAGAAACCATGCAAAGTCTCAGAATATACAAGTAC	SEQ ID NO:2	(260)	TC	AA	AC											AG			ΑT	T <sub>.</sub> G	CC	CA	AG	GC	C	TCC
(313)313320330340350364SEQ ID NO:1(288)AAAATGATTTTTTACAAAATGAAAAGAAAGTTGGACCATGGTTCTGAGGTCCSEQ ID NO:2(310)CTTTTTGTCGAAGACGGA-TGAAAAGAAAGTTGGACCATGGTTCTGAGGTCC(313)TTACATGAAAAGAAAGTTGGACCATGGTTCTGAGGTCCConsensus(313)TTACATGAAAAGAAAGTTGGACCATGGTTCTGAGGTCCSection 8(365)365370380390400416SEQ ID NO:1(340)GCTCTTTTTCTTTGGGAAAGAAACCATGCAAAGTCTCAGAATATACAAGTACSEQ ID NO:2(361)GCTCTTTTTCTTTGGGAAAGAAACCATGCAAAGTCTCAGAATATACAAGTAC	Consensus	(261)	ż	ΑA	С		ΤG	A G		GA	A	I	ΤA			Α	А	Т		Т	С	Α	G	GC		Т
SEQ ID NO:2       (310) CTTTTTGTCGAAGACGGA-TGAAAAGAAGTTGGACCATGGTTCTGAGGTCC         Consensus       (313)       T       T       AC       A       TGAAAAGAAGTTGGACCATGGTTCTGAGGTCC         Section 8         (365)       365       370       380       390       400       416         SEQ ID NO:1         SEQ ID NO:1       (340)       GCTCTTTTTCTTGGGAAAGAAACCATGCAAAGTCTCAGAATATACAAGTAC         SEQ ID NO:2       (361)       GCTCTTTTTCTTTGGGAAAGAAACCATGCAAAGTCTCAGAATATACAAGTAC																										-
SEQ ID NO:2       (310) CTTTTTGTCGAAGACGGA-TGAAAAGAAGTTGGACCATGGTTCTGAGGTCC         Consensus       (313)       T       T       AC       A       TGAAAAGAAGTTGGACCATGGTTCTGAGGTCC         Section 8         (365)       365       370       380       390       400       416         SEQ ID NO:1         SEQ ID NO:1       (340)       GCTCTTTTTCTTGGGAAAGAAACCATGCAAAGTCTCAGAATATACAAGTAC         SEQ ID NO:2       (361)       GCTCTTTTTCTTTGGGAAAGAAACCATGCAAAGTCTCAGAATATACAAGTAC		(313)	<u>313</u>			32	20				<u>330</u>				<u></u> 3-	40				_35	0					364
SEQ ID NO:2       (310) CTTTTTGTCGAAGACGGA-TGAAAAGAAGTTGGACCATGGTTCTGAGGTCC         Consensus       (313)       T       T       AC       A       TGAAAAGAAGTTGGACCATGGTTCTGAGGTCC         Section 8         (365)       365       370       380       390       400       416         SEQ ID NO:1         SEQ ID NO:1       (340)       GCTCTTTTTCTTGGGAAAGAAACCATGCAAAGTCTCAGAATATACAAGTAC         SEQ ID NO:2       (361)       GCTCTTTTTCTTTGGGAAAGAAACCATGCAAAGTCTCAGAATATACAAGTAC	' SEQ ID NO:1	(288)	AA	AA	ΤG	ΑT	ТΤ	ТТТ	AC	AA	AA?	TG.	AA	AA	GAA	AG	ΤТ	GG	AC	CA'	ΓG	GT	тС	ΤG	AGG	TCC
Section 8         (365)       365       370       380       390       400       416         SEQ ID NO:1       (340)       GCTCTTTTTCTTTGGGAAAGAAACCATGCAAAGTCTCAGAATATACAAGTAC         SEQ ID NO:2       (361)       GCTCTTTTTCTTTGGGAAAGAAACCATGCAAAGTCTCAGAATATACAAGTAC	SEQ ID NO:2	(310)	CT	ΤТ	ТΤ	GT	CG.	AAG	AC	GG	A-:	TG.	AAZ	AA	GAA	AG	ΤТ	GG	AC	CA'	ΓG	GΤ	ТC	ΤG	AGG	TCC
(365)365370380390400416SEQ ID NO:1(340)GCTCTTTTTCTTTGGGAAAGAAACCATGCAAAGTCTCAGAATATACAAGTACSEQ ID NO:2(361)GCTCTTTTTCTTTGGGAAAGAAACCATGCAAAGTCTCAGAATATACAAGTAC	Consensus	(313)			т	Т			AC		A 🛛	ΓG.	AAA	AA	GAA	AG	ΤТ	GG	AC	CA	ΓG					
SEQ ID NO:1 (340) GCTCTTTTTCTTTGGGAAAGAAACCATGCAAAGTCTCAGAATATACAAGTAC SEQ ID NO:2 (361) GCTCTTTTTCTTTGGGAAAGAAACCATGCAAAGTCTCAGAATATACAAGTAC													-												Sect	ion 8
SEQ ID NO:2 (361) GCTCTTTTTCTTTGGGAAAGAAACCATGCAAAGTCTCAGAATATACAAGTAC		• •																	-							
Consensus (365) GCTCTTTTTCTTTGGGAAAGAAACCATGCAAAGTCTCAGAATATACAAGTAC	•																									
	Consensus	(365)	GC	гС	ТΤ	ΤТ	TC	ттт	GG	GA	AA	GA.	AAC	cci	ATG	CA	AA	GT	СТ	CA	GA.	ΑТ	ΑT	AC	AAG	TAC

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(417)         (430         (40         (450         (468)           SEQ ID NO:1         (392)         CACTGGGCTTGTACCATGTTCAGCAACACCCAACAACTTTTGGGGACCTCAGA CONSENSUS         (417)         CACTGGGCTTGTACCATGTTCAGCAACACCAACAACTTTTGGGGACCTCAGA CONSENSUS         (417)         CACTGGGCTTGTACCATGTTCAGCAACACCAACAACAACTTTTGGGGACCTCAGA CONSENSUS         Section 10         Section 10           (469)         469         480         490         500         510         520           SEQ ID NO:1         (444)         GCAGCCAATGGCCAAGGGCAACAACGACGCCGAATTACATCTGTCCAGCCAC Consensus         (469)         GCAGCCAATGGCCAAGGGCAACAACGACGCCGAATTACATCTGTCCAGCCAC Consensus         (469)         CAGCCAATGGCCAAGGGCAACAACGACGCGGAATTACATCTGTCCAGCCAC Consensus         (469)         CAGCCCAATGGCCAAGGGCAACAACGACGCGGAATTACATCTGTCCAGCCAC Consensus         (521)         510         550         560         572           SEQ ID NO:1         (496)         CTACAGGCCTCCAGGAATGGCTAAAAATGTTCCAGGCTGGACGGAC											— Section 9	
SEQ ID NO:2       (413) CACTGGGCTTGTACCATGTTCAGCAACACCAACAACTTTTGGGGACCTCAGA         Section 10       Section 10         (469) 469       480       490       500       510       520         SEQ ID NO:1       (444) GCAGCCAATGGCCAAGGGCAACAACGACGCGCAATTACATCTGTCCAGCCAC       Section 10         (469) 469       480       490       500       510       520         SEQ ID NO:1       (444) GCAGCCAATGGCCAAGGGCAACAACGACGCCGAATTACATCTGTCCAGCCAC       Section 11       Section 12         (521) 521       530       540       550       560       572         SEQ ID NO:1       (496) CTACAGGCCTCCAGGAATGGCTAAAAATGTTTCAGAGCTGGAGTGGACCAGA       Section 11       Section 12         (521) 521       530       540       550       560       572         SEQ ID NO:1       (496) CTACAGGCCTCCAGGAATGGCTAAAAATGTTTCAGAGCTGGAGCGGACCAGA       Section 12       Section 12         (573) 573       573       580       590       600       610       624         SEQ ID NO:1       (548) GAAATTGCTTGCTTTTAGATGATCTATTGATGTGTGAACCAACAAGAGA       Section 13       Section 13       Section 14         (625) 625       630       640       650       660       676       SEQ ID NO:1       (610) AAACATATGATGATGATGATAGAACCCACAGTTCATTCAT		(417)	417		430		,440		,450		468	
SEQ ID NO:2       (413) CACTGGGCTTGTACCATGTTCAGCAACACCAACAACTTTTGGGGACCTCAGA         Section 10	SEQ ID NO:1	(392)	CACTGG	GCTTGT	ACCAT	GTTC	AGCAA	CACCAA	CAACI	TTTGGGG	ACCTCAGA	
Section 10         Section 10           SEQ ID NO:1         (449)         490         500         510         520           SEQ ID NO:2         (465)         GCAGCCAATGGCCAAGGGCAACAACGACGCCGAATTACATCTGTCCAGCCAC         Section 11           Consensus         (469)         GCAGCCCAATGGCCAAGGGCAACAACGACGCCGAATTACATCTGTCCAGCCAC         Section 11           (521)         521         530         540         550         560         572           SEQ ID NO:1         (496)         CTACAGGCCTCCAGGAATGGCTAAAAATGTTTCAGAGCTGGAGTGGACCAGA         Section 11         Section 11           (521)         521         CTACAGGCCTCCAGGAATGGCTAAAAATGTTTCAGAGCTGGAGTGGACCAGA         Consensus         (521)         CTACAGGCCTCCAGGAATGGCTAAAAATGTTCAGAGGCTGGAGCGGAGCAGAG           (521)         CTACAGGCCTCCAGGAATGGCTAAAAATGTTCCAGGAGCTGGAGCGAGC	SEQ ID NO:2											
(469)         460         490         500         510         520           SEQ ID NO:1         (444)         GCAGCCAATGGCCAAGGGCAACAACGACGCCGAATTACATCTGTCCAGCCAC           Consensus         (469)         GCAGCCAATGGCCAAGGGCAACAACGACGCCGAATTACATCTGTCCAGCCAC           Consensus         (469)         GCAGCCCAATGGCCAAGGGCAACAACGACGCCGAATTACATCTGTCCAGCCAC           SEQ ID NO:2         (45)         GCAGCCACGGCATGGCAACGACGCCGAATTACATCTGTCCAGCCAG	Consensus	(417)	CACTGG	GCTTGT	ACCAT	GTTCA	AGCAA	CACCAA	CAACI	TTTGGGG	ACCTCAGA	
SEQ ID NO:1       (444)       GCAGCCAATGGCCAAGGGCAACAACGACGCCGAATTACATCTGTCCAGCCAC         SEQ ID NO:2       (465)       GCAGCCAATGGCCAAGGGCAACAACGACGACGACGACTACATCTGTCCAGCCAC         Consensus       (469)       GCAGCCAATGGCCAAGGGCAACAACGACGACGACGAATTACATCTGTCCAGCCAC         SEQ ID NO:1       (496)       CTACAGGCCTCCAGGAATGGCTAAAAATGTTCAGAGCTGGAGTGGACCAGA         SEQ ID NO:1       (496)       CTACAGGCCTCCAGGAATGGCTAAAAATGTTCCAGAGCTGGAGTGGACCAGA         SEQ ID NO:2       (517)       CTACAGGCCTCCAGGAATGGCTAAAAATGTTTCAGAGCTGGAGTGGACCAGA         Consensus       (521)       573       580       590       600       610       624         SEQ ID NO:2       (530)       573       580       590       600       610       624         SEQ ID NO:2       (540)       GAAATTGCTTGCTTTAGATGAACCATTGATAGTGTGAACCAACAAGTA       Section 12       560       56			. <u>.</u>								- Section 10	
SEQ ID NO:2       (465)       GCAGCCAATGGCCAAGGGCAACAACGACGCCGAATTACATCTGTCCAGCCAC         Consensus       (469)       GCAGCCAATGGCCAAGGGCAACAACGACGCCGAATTACATCTGTCCAGCCAC         SEQ ID N0:1       (496)       CTACAGGCCTCCAGGAATGGCTAAAAATGTTTCAGAGCTGGAGTGGACCAGA         SEQ ID N0:2       (517)       CTACAGGCCTCCAGGAATGGCTAAAAATGTTTCAGAGCTGGAGTGGACCAGA         Consensus       (521)       CTACAGGCCTCCAGGAATGGCTAAAAATGTTTCAGAGCTGGAGTGGACCAGA         Consensus       (521)       CTACAGGCCTCCAGGAATGGCTAAAAATGTTCAGAGCTGGAGTGGACCAGA         Consensus       (521)       CTACAGGCCTCCAGGAATGGCTAAAAATGTTCAGAGCTGGAGTGGACCAGA         Consensus       (521)       CTACAGGCCTCCAGGAATGGCTAAAAATGTTCAGAGCTGGAGCAACAGA         SEQ ID N0:1       (548)       GAAATTGCTTGCTTTAGATGAACTCATTGATAGTGTGGAACCAACAAAGTA         SEQ ID N0:1       (569)       GAAATTGCTTGCTTTAGATGAACTCATTGATAGTGTGGAACCAACAAAGTA         SEQ ID N0:1       (600)       AAACATATGATGCAAGTGATAGAACCCCAGTTTCAACGAGACTCATTCAT		(469)	469			. 4	90					
SEQ ID NO:2       (465)       GCAGCCAATGGCCAAGGGCAACAACGACGCCGAATTACATCTGTCCAGCCAC         Consensus       (469)       GCAGCCAATGGCCAAGGGCAACAACGACGCCGAATTACATCTGTCCAGCCAC         SEQ ID N0:1       (496)       CTACAGGCCTCCAGGAATGGCTAAAAATGTTTCAGAGCTGGAGTGGACCAGA         SEQ ID N0:2       (517)       CTACAGGCCTCCAGGAATGGCTAAAAATGTTTCAGAGCTGGAGTGGACCAGA         Consensus       (521)       CTACAGGCCTCCAGGAATGGCTAAAAATGTTTCAGAGCTGGAGTGGACCAGA         Consensus       (521)       CTACAGGCCTCCAGGAATGGCTAAAAATGTTCAGAGCTGGAGTGGACCAGA         Consensus       (521)       CTACAGGCCTCCAGGAATGGCTAAAAATGTTCAGAGCTGGAGTGGACCAGA         Consensus       (521)       CTACAGGCCTCCAGGAATGGCTAAAAATGTTCAGAGCTGGAGCAACAGA         SEQ ID N0:1       (548)       GAAATTGCTTGCTTTAGATGAACTCATTGATAGTGTGGAACCAACAAAGTA         SEQ ID N0:1       (569)       GAAATTGCTTGCTTTAGATGAACTCATTGATAGTGTGGAACCAACAAAGTA         SEQ ID N0:1       (600)       AAACATATGATGCAAGTGATAGAACCCCAGTTTCAACGAGACTCATTCAT	SEQ ID NO:1	(444)	GCAGCC	AATGGC	CAAGG	GCAAC	CAACG	ACGCCG	AATTA	CATCTGT	CCAGCCAC	
Section 11           SEQ ID NO:1         (496)         CTACAGGCCTCCAGGAATGCCTAAAAATGTTTCAGAGCTGGACCAGA           SEQ ID NO:2         (517)         CTACAGGCCTCCAGGAATGCCTAAAAATGTTTCAGAGCTGGACCAGA           Consensus         (521)         CTACAGGCCTCCAGGAATGCCTAAAAATGTTTCAGAGCTGGACCAGA           Consensus         (521)         CTACAGGCCTCCAGGAATGCCTAAAAATGTTCCAGAGCTGGACCAGA           Consensus         (521)         CTACAGGCCTCCAGGAATGCCTAAAAATGTTCCAGAGCTGGACCAAGA           Section 12         Section 12         Section 12           (573)         573         580         590         600         610         624           SEQ ID NO:1         (548)         GAAATTGCTTGCTTTAGATGAACTCATTGATAGTTGTGAACCAACAAAGTA         Consensus         (573)         GAAATTGCTTGCTTTAGATGAACTCATTGATAGTAGTGGAACCAACAAGATA           SEQ ID NO:1         (540)         GAAT         GAA         650         660         676           SEQ ID NO:2         (621)         AAACATATGATGCAAGTGATAGAACCCAGTTTCAACGAGACTCAATTCAT         Section 13           SEQ ID NO:1         (600)         AAACATATGATGCAAGTGATAGAACCCCAGTTTCAACGAGACTCAATTCAT           SEQ ID NO:2         (621)         AAACATATGATGAAGTGGCAACTCATTGTGTTTCAACGAGACTCAATGAACCCAAAGA           SEQ ID NO:1         (652)         TGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAACCCAAAGA <t< td=""><td>SEQ ID NO:2</td><td>(465)</td><td>GCAGCC</td><td>AATGGC</td><td>CAAGG</td><td>GCAAC</td><td>CAACG</td><td>ACGCCG</td><td>AATTA</td><td>CATCIGI</td><td>CCAGCCAC</td></t<>	SEQ ID NO:2	(465)	GCAGCC	AATGGC	CAAGG	GCAAC	CAACG	ACGCCG	AATTA	CATCIGI	CCAGCCAC	
(521)         521         530         540         550         560         572           SEQ ID NO:1         (496)         CTACAGGCCTCCAGGAATGGCTAAAAATGTTTCAGAGCTGGAGTGGACCAGA           SEQ ID NO:2         (517)         CTACAGGCCTCCAGGAATGGCTAAAAATGTTTCAGAGCTGGAGTGGACCAGA           Section 12	Consensus	(469)	GCAGCC	AATGGC	CAAGG	GCAAC	CAACG	ACGCCG	AATTA	CATCTGT	CCAGCCAC	
SEQ ID NO:1       (496)       CTACAGGCCTCCAGGAATGGCTAAAAATGTTTCAGAGCTGGAGTGGACCAGA         SEQ ID NO:2       (517)       CTACAGGCCTCCAGGAATGGCTAAAAATGTTTCAGAGCTGGAGTGGACCAGA         Consensus       (521)       CTACAGGCCTCCAGGAATGGCTAAAAATGTTCAGAGCTGGAGTGGACCAGA         SEQ ID NO:1       (548)       GAAATTGCTTGCTTTAGATGAACTCATTGATAGTTGTGAACCAACACAAGTA         SEQ ID NO:2       (569)       GAAATTGCTTGCTTTAGATGAACTCATTGATAGTTGTGAACCAACACAAGTA         SEQ ID NO:2       (569)       GAAATTGCTTGCTTTAGATGAACTCATTGATAGTGTGGAACCAACACAAGTA         Consensus       (573)       GAAATTGCTTGCTTTAGATGAACTCATTGATAGTGTGGAACCAACACAAGTA         SEQ ID NO:2       (625)       625       630       640       650       660       676         SEQ ID NO:1       (600)       AAACATATGATGCAAGTGATAGAACCCCAGTTTCAACGAGACTTCATTCA											- Section 11	
SEQ ID NO:2       (517) CTACAGGCCTCCAGGAATGGCTAAAAATGTTTCAGAGCTGGAGTGGACCAGA         Section 12       (521) CTACAGGCCTCCAGGAATGGCTAAAAATGTTTCAGAGCTGGAGTGGACCAGA         Section 12       (573) 573 580 590 600 610 624         SEQ ID NO:1       (548) GAAATTGCTTGCTTTAGATGAACTCATTGATAGTTGTGAACCAACAAGTA         SEQ ID NO:2       (569) GAAATTGCTTGCTTTAGATGAACTCATTGATAGTTGTGAACCAACAAAGTA         Consensus       (573) 625 630 640 650 660 676         SEQ ID NO:1       (600) AAACATATGATGCAAGTGGATAGAACCCCAGTTTCAACGAGACTTCATTCA		(521)	521	,530		540		550		560	572	
Consensus(521) CTACAGGCCTCCAGGAATGGCTAAAAATGTTTCAGAGCTGGAGTGGACCAGASection 12Section 12(573)573580590600610624SEQ ID NO:1(548)GAAATTGCTTGCTTTAGATGAACTCATTGATAGTTGTGAACCAACAAAGTAConsensus(573)GAAATTGCTTGCTTTAGATGAACTCATTGATAGTTGTGAACCAACACAAGTAConsensus(573)GAAATTGCTTGCTTTAGATGAACTCATTGATAGTTGTGAACCAACACAAGTAConsensus(573)GAAATTGCTTGCTTTAGATGAACCCCACTTTCAACGAGACTTCATTCA	SEQ ID NO:1	(496)	CTACAG	GCCTCC	AGGAA	TGGCI	AAAA	ATGTTT	CAGAG	CTGGAGT	GGACCAGA	
Section 12 (573) 573 580 590 600 610 624 SEQ ID NO:1 (548) GAAATTGCTTGCTTTAGATGAACTCATTGATAGTTGTGAACCAACACAAGTA SEQ ID NO:2 (569) GAAATTGCTTGCTTTAGATGAACTCATTGATAGTTGTGAACCAACAAGTA Consensus (573) GAAATTGCTTGCTTTAGATGAACTCATTGATAGTTGTGAACCAACAAGTA (625) 625 630 640 650 660 676 SEQ ID NO:1 (600) AAACATATGATGCAAGTGATAGAACCCCAGTTTCAACGAGACTTCATTCA	SEQ ID NO:2											
(573)573580590600610624SEQ ID NO:1(548)GAAATTGCTTGCTTTAGATGAACTCATTGATAGTTGTGAACCAACAAGTASEQ ID NO:2(569)GAAATTGCTTGCTTTAGATGAACTCATTGATAGTTGTGAACCAACAAAGTAConsensus(573)GAAATTGCTTGCTTTAGATGAACTCATTGATAGTTGTGAACCAACAAAGTASEQ ID NO:1(600)AAACATATGCTGCAAGTGAAAGTGGAAACCCCAGTTTCAACGAGACTTCATTCA	Consensus	(521)	CTACAG	GCCTCC	AGGAA	TGGCI	AAAA	ATGTTT	CAGAC	CTGGAGT	GGACCAGA	
SEQ ID NO:1(548) GAAATTGCTTGCTTTAGATGAACTCATTGATAGTTGTGAACCAACACAAGTASEQ ID NO:2(569) GAAATTGCTTGCTTTAGATGATGAACTCATTGATAGTTGTGAACCAACACAAGTASection 13(625) 625 630 640 650 660 676SEQ ID NO:1(600) AAACATATGATGCAAGTGATAGAACCCAGTTCAACGAGACTTCATTCA											Section 12	
SEQ ID NO:2(569) GAAATTGCTTGCTTTAGATGAACTCATTGATAGTTGTGAACCAACACAAGTA ConsensusSection 13(625) 625 630 640 650 660 676SEQ ID NO:1(600) AAACATATGATGCAAGTGATAGAACCCCAGTTTCAACGAGACTTCATTCA		(573)	573	580		590		600		610	624	
Consensus(573)GAAATTGCTTGCTTTAGATGAACTCATTGATAGTTGTGAACCAACACAAGTASection 13(625)625630640650660676SEQ ID NO:1(600)AAACATATGATGCAAGTGATAGAACCCCAGTTTCAACGAGACTTCATTTCATSEQ ID NO:2(621)AAACATATGATGCAAGTGATAGAACCCCAGTTTCAACGAGACTTCATTTCATConsensus(625)AAACATATGATGCAAGTGATAGAACCCCAGTTTCAACGAGACTTCATTTCATSection 14(677)677690700710728SEQ ID NO:1(673)TGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAACCCAAAGAConsensus(677)TGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAACCCAAAGAConsensus(677)TGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAACCCAAAGASection 14(673)TGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAACCCAAAGAConsensus(677)TGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAACCCAAAGASection 15(729)740750760770780SEQ ID NO:1(704)CCTGCTACAAGCAGCTCAGACATGTCGCTACTGGAGAATTTTGGCTGAAGACSection 15(729)740750760770780SEQ ID NO:1(704)CCTGCTACAAGCAGCTCAGACATGTCGCTACTGGAGAATTTGGCTGAAGACSEQ ID NO:1(729)200810820832SEQ ID NO:1(751)781790800810820	SEQ ID NO:1	(548)	GAAATT	GCTTGC	TTTAG	ATGAA	CTCA	TTGATA	GTTGT	GAACCAA	CACAAGTA	
Section 13(625)625630640650660676SEQ ID NO:1(600)AAACATATGATGCAAGTGATAGAACCCCAGTTTCAACGAGACTTCATTTCATSEQ ID NO:2(621)AAACATATGATGCAAGTGATAGAACCCCAGTTTCAACGAGACTTCATTTCATConsensus(625)AAACATATGATGCAAGTGATAGAACCCCAGTTTCAACGAGACTTCATTTCATConsensus(625)AAACATATGATGCAAGTGGCACTCTATGTGCTTTCAACGAGACTTCATTTCATSEQ ID NO:1(652)TGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAACCCAAAGASEQ ID NO:2(673)TGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAACCCCAAAGASEQ ID NO:2(677)TGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAACCCAAAGASEQ ID NO:2(729)729740720760770780SEQ ID NO:1(704)CCTGCTACAAGCAGCTCAGACATGTCGCTACTGGAGAATTTTGGCTGAAGACSEQ ID NO:2(725)CCTGCTACAAGCAGCTCAGACATGTCGCTACTGGAGAATTTTGGCTGAAGACSEQ ID NO:2(721)781790800810820SEQ ID NO:1(756)AACCTTCTCTGGAGAGAGAAATGCAAAGAAGAGGGGATTGATGAACCATTGCSEQ ID NO:1(756)AACCTTCTCTGGAGAGAGAAATGCAAAGAAGAGAGGGGATTGATGAACCATTGCSEQ ID NO:1(756)AACCTTCTCTGGAGAGAGAAATGCAAAGAAGAAGAGGGGATTGATGAACCATTGCSEQ ID NO:1(756)AACCTTCTCTGGAGAGAGAAATGCAAAGAAGAAGAGGGGATTGATGAACCATTGCSEQ ID NO:1(756)AACCTTCTCTGGAGAGAGAAATGCAAAGAAGAAGAGGGGATTGATGAACCATTGCSEQ ID NO:2(777)AACCTTCTCTGGAGAGAGAAATGCAAAGAAGAAGAGGGGATTGATGAACCATTGC	SEQ ID NO:2	(569)	GAAATT	GCTTGC	TTTAG.	ATGAA	CTCA	TTGATA	GTTGI	GAACCAA	CACAAGTA	
(625)625630640650660676SEQ ID NO:1(600)AAACATATGATGCAAGTGATAGAACCCCAGTTTCAACGAGACTTCATTTCATSEQ ID NO:2(621)AAACATATGATGCAAGTGATAGAACCCCAGTTTCAACGAGACTTCATTTCATConsensus(625)AAACATATGATGCAAGTGATAGAACCCCAGTTTCAACGAGACTTCATTTCAT(625)AAACATATGATGCAAGTGGCAACTCTATGTGCTTTCAACGAGACTTCATTTCAT(627)677690700710728SEQ ID NO:1(652)TGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAACCCAAAGASEQ ID NO:2(673)TGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAACCCAAAGASEQ ID NO:1(704)CCTGCTACAAGCAGCTCAGACATGTCGCTACTGGAGAATTTTGGCTGAAGACSEQ ID NO:1(704)CCTGCTACAAGCAGCTCAGACATGTCGCTACTGGAGAATTTTGGCTGAAGACSEQ ID NO:2(729)CCTGCTACAAGCAGCTCAGACATGTCGCTACTGGAGAATTTTGGCTGAAGACSEQ ID NO:1(781)781790800810820832SEQ ID NO:1(756)AACCTTCTCTGGAGAGAAATGCAAAGAAGAGGGGGATTGATGAACCATTGCSEQ ID NO:2(777)AACCTTCTCTGGAGAGAGAAATGCAAAGAAGAGAGGGGATTGATGAACCATTGCSEQ ID NO:1(756)AACCTTCTCTGGAGAGAGAAATGCAAAGAAGAAGAGGGGATTGATGAACCATTGCSEQ ID NO:2(777)AACCTTCTCTGGAGAGAGAAATGCAAAGAAGAAGAGGGGATTGATGAACCATTGC	Consensus	(573)	GAAATT	GCTTGC	TTTAG	ATGAA	CTCA	TTGATA	GTTGI	GAACCAA	CACAAGTA	
SEQ ID NO:1(600)AAACATAT GAT GCAAGT GAT AGAACCCC AGT TT CAACGA GACTT CAT TT CATSEQ ID NO:2(621)AAACAT AT GAT GCAAGT GAT AGAACCCC AGT TT CAACGA GACTT CAT TT CATConsensus(625)AAACAT AT GAT GCAAGT GAT AGAACCCC AGT TT CAACGA GACT TC AT TT CATConsensus(625)AAACAT AT GAT GCAAGT GAT AGAACCCC AGT TT CAACGA GACT TC AT TT CATSEQ ID NO:1(677)677690700710728SEQ ID NO:2(652)TGCTCCCT AAAGAGT TGGCACT CT AT GT GCT TT CAT TC CT GGAACCCAAAGASEQ ID NO:2(673)TGCT CCCT AAAGAGT TGGCACT CT AT GT GCT TT CAT TC CT GGAACCCAAAGAConsensus(677)TGCT CCCT AAAGAGT TGGCACT CT AT GT GCT TT CAT TC CT GGAACCCAAAGASection 15SEQ ID NO:2(729)729740750760770780SEQ ID NO:1(704)CCT GCT ACAAGCAGCT CAGACAT GT CGCT ACT GGAGAAT TT T GGCT GAAGACSection 15SEQ ID NO:2(729)CCT GCT ACAAGCAGCT CAGACAT GT CGCT ACT GGAGAAT TT T GGCT GAAGACSection 16SEQ ID NO:1(781)781790800810820832SEQ ID NO:1(756)AACCTT CT CT GGAGAGAGAAAT GCAAAGAAGAGGGGGATT GAT GAACCAT TG CSection 16SEQ ID NO:1(756)AACCTT CT CT GGAGAGAGAAAT GCAAAGAAGAGGGGGAT TG AT GAACCAT TG CSection 16SEQ ID NO:2(777)AACCTT CT CT GGAGAGAGAAAT GCAAAGAAGAGGGGGAT TG AT GAACCAT TG CSEQ ID NO:1(756)AACCTT CT CT GGAGAGAGAAAT GCAAAGAAGAGGGGGAT TG AT GAACCAT TG CSEQ ID NO:2(777)AACCTT CT CT GGAGAGAGAAAT GCAAAGAAGAGGGGGAT TG AT GAACCAT TG C <td></td> <td> Section 13</td>											Section 13	
SEQ ID NO:2(621) AAACATATGATGCAAGTGATAGAACCCCAGTTTCAACGAGACTTCATTTCAT (625) AAACATATGATGCAAGTGATAGAACCCCAGTTTCAACGAGACTTCATTTCAT Section 14(677)677690700710728SEQ ID NO:1(652) TGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAACCCAAAGA (673) TGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAACCCAAAGA (677) TGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAACCCAAAGA (677) TGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAACCCAAAGA (677) TGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAACCCAAAGA (677) TGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAACCCAAAGA (677) TGCTCCTACAAGCAGCTCAGACATGTCGCTACTGGAGAATTTTGGCTGAAGAC Section 15SEQ ID NO:1(704) CCTGCTACAAGCAGCTCAGACATGTCGCTACTGGAGAATTTTGGCTGAAGAC Consensus790800810820832SEQ ID NO:1781790800810820832SEQ ID NO:1(756) AACCTTCTCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG		(625)	625 63	30	,640		,65	50	660	)	676	
Consensus(625) AAACATATGATGCAAGTGATAGAACCCCAGTTTCAACGAGACTTCATTTCAT(677)677690700710728SEQ ID NO:1(652)TGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAACCCAAAGASEQ ID NO:2(673)TGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAACCCAAAGAConsensus(677)TGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAACCCAAAGASEQ ID NO:2(729)729740750760770780SEQ ID NO:1(704)CCTGCTACAAGCAGCTCAGACATGTCGCTACTGGAGAATTTTGGCTGAAGACSection 15Section 15SEQ ID NO:2(725)CCTGCTACAAGCAGCTCAGACATGTCGCTACTGGAGAATTTTGGCTGAAGACSection 16(781)781790800810820832SEQ ID NO:1(756)AACCTTCTCTGGAGAGAGAGAGAGAAATGCAAAGAAGAGGGGATTGATGAACCATTGCSEQ ID NO:1(756)AACCTTCTCTGGAGAGAGAAATGCAAAGAAGAGGGGATTGATGAACCATTGCSEQ ID NO:2(777)AACCTTCTCTGGAGAGAGAAATGCAAAGAAGAGGGGATTGATGAACCATTGCSEQ ID NO:2(777)AACCTTCTCTGGAGAGAGAAATGCAAAGAAGAGGGGATTGATGAACCATTGC	SEQ ID NO:1	(600)	AAACAT	ATGATG	CAAGT	GATAG	AACC	CCAGTT	TCAAC	GAGACTT	CATTTCAT	
Section 14(677)677690700710728SEQ ID NO:1(652)TGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAACCCAAAGASEQ ID NO:2(673)TGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAACCCAAAGAConsensus(677)TGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAACCCAAAGASEQ ID NO:1(729)729740750760770780SEQ ID NO:2(720)729740750760770780SEQ ID NO:2(725)CCTGCTACAAGCAGCTCAGACATGTCGCTACTGGAGAATTTTGGCTGAAGACSection 15Consensus(729)CCTGCTACAAGCAGCTCAGACATGTCGCTACTGGAGAATTTGGCTGAAGACSection 16SEQ ID NO:2(781)781790800810820832SEQ ID NO:1(756)AACCTTCTCTGGAGAGAGAAATGCAAAGAAGAAGAGGGGATTGATGAACCATTGCSEQ ID NO:2(777)AACCTTCTCTGGAGAGAGAAATGCAAAGAAGAAGAGGGGATTGATGAACCATTGC	•											
SEQ ID NO:1(677)690700710728SEQ ID NO:2(652)TGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAACCCAAAGASEQ ID NO:2(673)TGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAACCCAAAGA(677)TGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAACCCAAAGA(677)TGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAACCCAAAGA(677)TGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAACCCAAAGA(677)TGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAACCCAAAGA(677)TGCTCCCTACAAGCAGCTCAGACATGTCGCTACTGGAAGAATTTGGCTGAAGACSEQ ID NO:1(704)CCTGCTACAAGCAGCTCAGACATGTCGCTACTGGAGAATTTTGGCTGAAGACSEQ ID NO:2(729)CCTGCTACAAGCAGCTCAGACATGTCGCTACTGGAGAAATTTGGCTGAAGAC(781)781790800810820820832SEQ ID NO:1(756)AACCTTCTCTGGAGAGAGAAATGCAAAGAAGAGGGGATTGATGAACCATTGCSEQ ID NO:2(777)AACCTTCTCTGGAGAGAGAAATGCAAAGAAGAGGGGGATTGATGAACCATTGC	Consensus	(625)	AAACAT	ATGATG	CAAGT	GATAG	SAACC	CCAGTT	TCAAC	GAGACTT		
SEQ ID NO:1(652)TGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAACCCAAAGASEQ ID NO:2(673)TGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAACCCAAAGAConsensus(677)TGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAACCCAAAGASection 15(729)729740750760770780Section 15Section 15(729)729740750760770780Section 15Section 15SEQ ID NO:1(704)CCTGCTACAAGCAGCTCAGACATGTCGCTACTGGAGAATTTTGGCTGAAGACConsensus(729)CCTGCTACAAGCAGCTCAGACATGTCGCTACTGGAGAATTTTGGCTGAAGACSection 16(781)781790800810820832SEQ ID NO:1(756)ACCTTCTCTGGAGAGAGAGAGAGAGAGAGAGAGAGGGGATTGATGAACCATTGCSEQ ID NO:1(777)ACCTTCTCTGGAGAGAGAGAGAGAGAGAGAGAGAGGGGATTGATGAACCATTGCSEQ ID NO:1(776)ACCTTCTCTGGAGAGAGAGAGAGAGAGAGAGAGGGGATTGATGAACCATTGCSEQ ID NO:1(781)790800810820832SEQ ID NO:1(781) <td colsp<="" td=""><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td>— Section 14</td></td>	<td></td> <td>— Section 14</td>											— Section 14
SEQ ID NO:2       (673) TGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAACCCCAAAGA         Consensus       (677) TGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAACCCCAAAGA         Section 15       Section 15         (729)       729       740       750       760       770       780         SEQ ID NO:1       (704)       CCTGCTACAAGCAGCTCAGACATGTCGCTACTGGAGAATTTTGGCTGAAGAC       SEQ ID NO:2       (725)       CCTGCTACAAGCAGCTCAGACATGTCGCTACTGGAGAATTTTGGCTGAAGAC         SEQ ID NO:2       (729)       CCTGCTACAAGCAGCTCAGACATGTCGCTACTGGAGAATTTTGGCTGAAGAC       Section 16         (781)       781       790       800       810       820       832         SEQ ID NO:1       (756)       AACCTTCTCTGGAGAGAGAGAAATGCAAAGAAGAGGGGGATTGATGAACCATTGC       SEQ ID NO:2       (777)       AACCTTCTCTGGAGAGAGAGAAATGCAAAGAAGAGGGGGATTGATGAACCATTGC												
Consensus(677) TGCTCCCTAAAGAGTTGGCACTCTATGTGCTTTCATTCCTGGAACCCCAAAGASection 15Section 15(729) 729740750760770780SEQ ID NO:1(704) CCTGCTACAAGCAGCTCAGACATGTCGCTACTGGAGAATTTTGGCTGAAGACSEQ ID NO:2(725) CCTGCTACAAGCAGCTCAGACATGTCGCTACTGGAGAATTTTGGCTGAAGACConsensus(729) CCTGCTACAAGCAGCTCAGACATGTCGCTACTGGAGAATTTTGGCTGAAGACSection 16(781) 781790800810820832SEQ ID NO:1(756) AACCTTCTCTGGAGAGAGAGAGAGAGAGAGAGAGGGGGATTGATGAACCATTGCSEQ ID NO:2(777) AACCTTCTCTGGAGAGAGAGAGAAATGCAAAGAAGAGGGGGATTGATGAACCATTGC	•											
Section 15         (729)       729       740       750       760       770       780         SEQ ID NO:1       (704)       CCTGCTACAAGCAGCTCAGACATGTCGCTACTGGAGAATTTTGGCTGAAGAC         SEQ ID NO:2       (725)       CCTGCTACAAGCAGCTCAGACATGTCGCTACTGGAGAATTTTGGCTGAAGAC         Consensus       (729)       CCTGCTACAAGCAGCTCAGACATGTCGCTACTGGAGAATTTTGGCTGAAGAC         SEQ ID NO:2       (781)       781       790       800       810       820       832         SEQ ID NO:1       (756)       AACCTTCTCTGGAGAGAGAAATGCAAAGAAGAGGGGGATTGATGAACCATTGC       SEQ ID NO:2       (777)       AACCTTCTCTGGAGAGAGAAATGCAAAGAAGAGGGGGATTGATGAACCATTGC	SEQ ID NO:2											
(729)729740750760770780SEQ ID NO:1(704)CCTGCTACAAGCAGCTCAGACATGTCGCTACTGGAGAATTTTGGCTGAAGACSEQ ID NO:2(725)CCTGCTACAAGCAGCTCAGACATGTCGCTACTGGAGAATTTTGGCTGAAGAC(729)CCTGCTACAAGCAGCTCAGACATGTCGCTACTGGAGAATTTTGGCTGAAGAC(729)CCTGCTACAAGCAGCTCAGACATGTCGCTACTGGAGAATTTTGGCTGAAGAC(729)CCTGCTACCAGGAGAGCAGCATGTCGCTACTGGAGAATTTTGGCTGAAGAC(729)CCTGCTACCAGCAGCTCAGACATGTCGCTACTGGAGAGAGA	Consensus	(677)	TGCTCC	CTAAAG.	AGTTG	GCACI	CTAT	GTGCTT	TÇATT	CCTGGAA	CCCAAAGA	
SEQ ID NO:1       (704)       CCTGCTACAAGCAGCTCAGACATGTCGCTACTGGAGAATTTTGGCTGAAGAC         SEQ ID NO:2       (725)       CCTGCTACAAGCAGCTCAGACATGTCGCTACTGGAGAATTTTGGCTGAAGAC         Consensus       (729)       CCTGCTACAAGCAGCTCAGACATGTCGCTACTGGAGAATTTTGGCTGAAGAC         Section 16         (781)         781       790       800       810       820       832         SEQ ID NO:1         SEQ ID NO:2       (776)       AACCTTCTCTGGAGAGAGAGAGAGAGAGAGGGGGATTGATGAACCATTGC											— Section 15	
SEQ ID NO:2       (725) CCTGCTACAAGCAGCTCAGACATGTCGCTACTGGAGAATTTTGGCTGAAGAC         Consensus       (729) CCTGCTACAAGCAGCTCAGACATGTCGCTACTGGAGAATTTTGGCTGAAGAC         Section 16         (781) 781 790 800 810 820 832         SEQ ID NO:1         SEQ ID NO:1         SEQ ID NO:1         SEQ ID NO:1         SEQ ID NO:2         (777) AACCTTCTCTGGAGAGAGAGAGAGAGAGAGAGGGGGATTGATGAACCATTGC										-		
Consensus       (729)       CCTGCTACAAGCAGCTCAGACATGTCGCTACTGGAGAATTTTGGCTGAAGAC         Section 16         (781)       781       790       800       810       820       832         SEQ ID NO:1         SEQ ID NO:2       (777)       AACCTTCTCTGGAGAGAGAGAGAGAGAGAGGGGGATTGATGAACCATTGC	SEQ ID NO:1	(704)	CCTGCT	ACAAGC	AGCTC	AGACA	TGTC	GCTACT	GGAGA	ATTTTGG	CTGAAGAC	
Section 16         (781)       781       790       800       810       820       832         SEQ ID NO:1       (756)       AACCTTCTCTGGAGAGAGAGAGAGAGAGAGGGGGATTGATGAACCATTGC         SEQ ID NO:2       (777)       AACCTTCTCTGGAGAGAGAGAAATGCAAAGAAGAGGGGGATTGATGAACCATTGC	SEQ ID NO:2	(725)	CCTGCT	ACAAGC	AGCTC	AGACA	TGTC	GCTACT	GGAGA	ATTTTGG	CTGAAGAC	
(781)781790800810820832SEQ ID NO:1(756)AACCTTCTCTGGAGAGAGAGAGAGAGAGAGGGGGATTGATGAACCATTGCSEQ ID NO:2(777)AACCTTCTCTGGAGAGAGAGAAATGCAAAGAAGAGGGGGATTGATGAACCATTGC	Consensus	(729)	CCTGCT	ACAAGC	AGCTC	AGACA	TGTC	GCTACT	GGAGA	ATTTTGG	CTGAAGAC	
SEQ ID NO:1 (756) AACCTTCTCTGGAGAGAGAGAAATGCAAAGAAGAGGGGGATTGATGAACCATTGC SEQ ID NO:2 (777) AACCTTCTCTGGAGAGAGAGAAATGCAAAGAAGAGGGGGATTGATGAACCATTGC											- Section 16	
SEQ ID NO:2 (777) AACCTTCTCTGGAGAGAGAGAAATGCAAAGAAGAGGGGGATTGATGAACCATTGC		(781)	781	790		800		810		820	832	
	SEQ ID NO:1	(756)	AACCTT	CTCTGG	AGAGA	GAAAT	GCAA	AGAAGA	GGGGA	TTGATGA	ACCATTGC	
Consensus (781) AACCTTCTCTGGAGAGAGAGAAATGCAAAGAAGAGGGGATTGATGAACCATTGC	SEQ ID NO:2	(777)	AACCTT	CTCTGG	AGAGA	GAAAT	GCAA	AGÀAGA	GGGGA	TTGATGA	ACCATTGC	
	Consensus	(781)	AACCTT	CTCTGG	AGAGA	GAAAT	GCAA	AGAAGA	GGGGA	TTGATGA	ACCATTGC	

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								——— Section 17
	(833)	833	,840	,8	50	860	870	884
SEQ ID NO:1	(808)	ACAT	TCAAGAG	AAGAAAAG	TAATAAA	ACCAGGI	TTCATACACA	AGTCCATGGAA
SEQ ID NO:2	(829)	ACAT	ICAAGAG	AAGAAAAG	TAATAAA	ACCAGGI	TTCATACACA	AGTCCATGGAA
Consensus	(833)	ACAT	TCAAGAG	AAGAAAAG	TAATAAA	ACCAGGI	TTCATACACA	GTCCATGGAA
								—— Section 18
	(885)	885	890	,900		910	920	936
SEQ ID NO:1								GCGAGGAGAA
SEQ ID NO:2								GCGAGGAGAA
Consensus	(885)	AAG	FGCATAC	ATCAGACA	GCACAGA	ATTGATA	CTAACTGGAG	GCGAGGAGAA
				··· ·· ·· · · ·· ·· ··		· · ·		Section 19
	(937)			,950	.960		970	988
SEQ ID NO:1	(912)	CTC	AAATCTC	CTAAGGTG	CTGAAAG	GACATGA	TGATCATGT	GATCACATGCT
SEQ ID NO:2								SATCACATGCT
Consensus	(937)	CTCI	AAATCTC	CTAAGGTG	CTGAAAG	GACATGA	TGATCATGT	GATCACATGCT
								——— Section 20
	(989)			,1000	,1010			030 1040
SEQ ID NO:1								ACACTTTAAA
SEQ ID NO:2								ACACTTTAAA
Consensus	(989)	TACA	AGTTTTG	TGGTAACC	GAATAGT	TAGTGGT	TCTGATGACA	ACACTTTAAA
				<u> </u>	<u></u>			Section 21
	(1041)			050	<u>,</u> 1060	1070		
SEQ ID NO:1	(1016)	AGTI	TGGTCA	GCAGTCAC	AGGCAAA	FGTCTGA	GAACATTAGI	GGGACATACA
								GGGACATACA
Consensus	(1041)	AGTI	TGGTCA	GCAGTCAC	AGGCAAA	IGTCTGA	GAACATTAGI	GGGACATACA
				<u> </u>				——— Section 22
	(1093)		,1100		110	,1120	,1130	1144
SEQ ID NO:1	(1068)	GGTG	GAGTAT	GGTCATCA	CAAATGA	GAGACAA	CATCATCATI	AGTGGATCTA
								AGTGGATCTA
Consensus	(1093)	GGTG	GGAGTAT	GGTCATCA	CAAATGA	GAGACAA	CATCATCATI	AGTGGATCTA
				······································				—— Section 23
	(1145)		1150			1170	,1180	1196
SEQ ID NO:1	(1120)	CAGA	TCGGAC	ACTCAAAG	TGTGGAA	FGCAGAG	ACTGGAGAAI	GTATACACAC
								GTATACACAC
Consensus	(1145)	CAGA	TCGGAC	ACTCAAAG	TGTGGAA	FGCAGAG	ACTGGAGAAI	GTATACACAC
								Section 24
	(1197)			,1210			,1230	1248
								TGAAAAAAGA
								TGAAAAAAGA
Consensus	(1197)	CTTA	TATGGG	CATACTTC	CACTGTG	CGTTGTA	TGCATCTTCA	TGAAAAAAGA

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		·····							- Section 25
(1249)	1249		1260		1270	,1	280	,1290	1300
SEQ ID NO:1 (1224)	GTTG	TTAGCG	GTTCT	CGAGAT	GCCAC	TCTTAG	GGTTTG	GGATAT	TGAGACAG
SEQ ID NO:2 (1245)	GTTG	TTAGCG	GTTCT	CGAGAT	GCCAC	TCTTAG	GGTTTG	GGATATT	FGAGACAG
Consensus (1249)									
<u></u>									- Section 26
(1301)	1301	,13	10	132	20	1330		,1340	1352
SEQ ID NO:1 (1276)	GCCA	GTGTTT	ACATG	TTTTGA	TGGGT	CATGTT	GCAGCA	GTCCGCT	TGTGTTCA
SEQ ID NO:2 (1297)	GCCA	GTGTTT	ACATG	TTTTGA	TGGGT	CATGTT	GCAGCA	GTCCGCT	TGTGTTCA
Consensus (1301)	GCCA	GTGTTT	ACATG	TTTTGA	TGGGT	CATGTT	GCAGCA	GTCCGC	GTGTTCA
<b></b>							·	• • .	- Section 27
(1353)	1353	,1360		,1370		1380	,1.	390	1404
SEQ ID NO:1 (1328)	ATAT	GATGGC	AGGAG	GGTTGT	TAGTG	GAGCAT	ATGATT	TTATGGT	TAAAGGTG
SEQ ID NO:2 (1349)									
Consensus (1353)	ATAT	GATGGC	AGGAG	GGTTGT	TAGTG	GAGCAT	ATGATT	TTATGGI	TAAAGGTG
·						·			- Section 28
(1405)	1405	1410		1420	,14	30	,1440		1456
SEQ ID NO:1 (1380)	TGGG	ATCCAG	AGACT	GAAACC	TGTCT	ACACAC	GTTGCA	GGGGCAT	TACTAATA
SEQ ID NO:2 (1401)	TGGG	ATCCAG	AGACT	GAAACC	TGTCTA	ACACAC	GTTGCA	GGGGCAI	TACTAATA
Consensus (1405)	TGGG	ATCCAG	AGACT	GAAACC	TGTCT	ACACAC	GTTGCA	GGGGCAI	TACTAATA
									- Section 29
(1457)			,147		1480		1490		1508
SEQ ID NO:1 (1432)	GAGT	CTATTC	ATTAC	AGTTTG	ATGGT	ATCÇAT	GTGGTG	AGTGGAI	CTCTTGA
SEQ ID NO:2 (1453)									
Consensus (1457)	GAGT	CTATTC	ATTAC	AGTTTG	ATGGT	ATCCAT	GTGGTG	AGTGGAT	CTCTTGA
									- Section 30
(1509)	1509		1520		1530		540	1550	1560
SEQ ID NO:1 (1484)	TACAT	FCAATCO	GTGT	TTGGGA	TGTGGA	AGACAG	GGAATT	GCATTCA	CACGTTA
SEQ ID NO:2 (1505)									
Consensus (1509)	TACAT	CAATCO	GTGT	TTGGGA	ŢĢŢGG	GACAG	GGAATT	GCATTCA	CACGTTA
								· · · · · · · · · · · · · · · · · · ·	– Section 31
(1561)						,1590		1600	1612
SEQ ID NO:1 (1536)									
SEQ ID NO:2 (1557)									
Consensus (1561)	ACAGO	GGCACCA	GTCG	TTAACA	AGTGGA	ATGGA.	ACTCAA	AGACAAI	ATTCTTG
			·- ··						- Section 32
(1613)		1620		1630		1640		550	1664
SEQ ID NO:1 (1588)	TCTCT	GGGAAI	GCAG	ATTCTA	CAGTTA	AAATC	TGGGAT	ATCAAAA	CAGGACA
SEQ ID NO:2 (1609)									
Consensus (1613)	TCTCI	GGGAAI	GCAG	ATTCTA	CAGTTA	AAATC	TGGGAT	АТСАААА	CAGGACA

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					·				- Section 33
	1665			680			1700		1716
SEQ ID NO:1 (1640)	GTGT	TTACA	AACATTO	GCAAGG	TCCCAA	CAAGCA	TCAGAGT	GCTGT	GACCTGT
SEQ ID NO:2 (1661)									
Consensus (1665)	GTGT	TTACA	AACATTO	CAAGG	TCCCAA	CAAGCA	TCAGAGT	GCTGT	GACCTGT
							<u>+</u> ,		- Section 34
(1717)			1730		1740		1750		1768
SEQ ID NO:1 (1692)									
SEQ ID NO:2 (1713)	TTAC	AGTTC	AACAAGA	ACTTT	GTAATT	ACCAGC	TCAGATG	ATGGA	ACTGTAA
Consensus (1717)	TTAC	AGTTC	AACAAGA	ACTTT	GTAATT	ACCAGC	TCAGATG	ATGGA	ACTGTAA
									- Section 35
(1769)	1769		1780		1790	,180	0	,1810	1820
SEQ ID NO:1 (1744)	AACT	ATGGG	ACTTGAA	AACGG	GTGAAT	TTATTC	GAAACCT	AGTCA	CATTGGA
SEQ ID NO:2 (1765)	AACT	ATGGG	ACTTGAA	AACGG	GTGAAT	TTATTC	GAAACCT	AGTCA	CATTGGA
Consensus (1769)	AACT	ATGGG	ACTTGAA	AACGG	GTGAAT	TTATTC	GAAACCT	AGTCA	CATTGGA
									- Section 36
(1821)	1821		1830	184	0	,1850	.1	860	1872
SEQ ID NO:1 (1796)									CACAAAG
SEQ ID NO:2 (1817)									
Consensus (1821)									
							•		- Section 37
(1873)	1873	,188	0	1890		1900	,1910		1924
SEQ ID NO:1 (1848)		TGTGT	GCAGTTO	GGAGT	CGGAAT	GGGACT	GAAGAAA	CCAÁG	CTGCTGG
SEQ ID NO:2 (1869)									
Consensus (1873)									
						÷.			Section 38
(1925)	1925	1930	.1	940	.195	0	,1960		1976
								GATGA	ATTTGTC
SEQ ID NO:1 (1900) SEQ ID NO:2 (1921)	TGCT	GGACT	TTGATGT	GGACA	FGAAGT	GAAGAG	CAGAAAA	GATGA	ATTTGTC
Consensus (1925)	TGCT	GGACT	TTGATGT	GGACA	IGAAGT	GAAGAG	CAGAAAA	GATGA	ATTTGTC
									Section 39
(1977)	1977		1990	I	2000	-	2010		2028
(1977) SEQ ID NO:1 (1952)	CAATT	TGTGT	AGACGAT	ATACTO			CCTGCA	AAAG	
SEQ ID NO:2 (1973)	CAATI	rgrgr)	AGACGAT	ATACTO	CCTGC		CCTGCA	AAAAG	
Consensus (1977)									
									Section 40
(2029)	2029		2040	2	2050	206	0	2070	2080
SEQ ID NO:1 (2004)		AGAAA							
SEQ ID NO:2 (2025)	GAAA	AGAAA	AAGAAAA	AAATCO	CTTGT	TCTCAG	IGGTGCA	GGATG	TTGGCTT
Consensus (2029)	GAAA	AGAAA	AAGAAAA	AAATCO	CCTTGT	TCTCAG	IGGTGCA	GGATG	TTGGCTT
								0	

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									- Section 41
(2081)	2081	20	)90	210	00	211	0	2120	2132
SEQ ID NO:1 (2056)	GGGG	CAACAG	ATTGAA	AAGAC	CTAC	AGACTA	AGAAGGA	AAGAA	GAAGAGAT
SEQ ID NO:1 (2056) SEQ ID NO:2 (2077)	GGGG	CAACAG	ATTGAA	AAGAC	CTAC	AGACTA	AGAAGGA	AAGAA	GAAGAGAT
Consensus (2081)	GGGG	CAACAG	ATTGAA	AAGAC	CTAC	AGACTA	AGAAGGA	AAGAA	GAAGAGAT
									- Section 42
(2133)	2133	2140				2160	21		2184
SEQ ID NO:1 (2108)					GAGG	CGTCTG			
SEQ ID NO:2 (2129)									
Consensus (2133)	GACA	AACCAT	AACTGA	CAAGA	GAGG	CGTCTG	CTGTCTCA	TCACA	TAAAAGGC
			· · · ··						– Section 43
	<u>2185</u>			200		2210	2220		2236
SEQ ID NO:1 (2160) SEQ ID NO:2 (2181)	TTCA	CTTTTG.	ACTGAG	GGCAG	CTTTO	GCAAAA?	IGAGACTI	TCTAA	ATCAAACC
SEQ ID NO:2 (2181)	TTCA	CTTTTG	ACTGAG	GGCAG	CTTT	GCAAAA?	IGAGACTI	TCTAA	ATCAAACC
Consensus (2185)	TTCA	CTTTTG	ACTGAG	GGCAG	CTTTC	GCAAAA	IGAGACTI	TCTAA	ATCAAACC
<u></u>									– Section 44
(2237) SEQ ID NO:1 (2212) SEQ ID NO:2 (2233)	2237		2250		2260	00	2270		2288
SEQ ID NO:1 (2212)	AGGT	GCAATT.	ATTTCT	TTATT	TTCT	CTCCA	GTGGTCAI	TGGGG	CAGTGTTA
SEQ ID NO:2 (2233)	AGGT	GCAATT.	ATTTCT	TTATT	TTCT	CTCCA	GTGGTCAI	TGGGGG	CAGTGTTA
Consensus (2237)	AGGT	GCAATT.	ATTTCT	TTATT	TTCT	CTCCA	GTGGTCAI	TGGGG	CAGTGTTA
			<i>i</i> '						- Section 45
(2289) SEQ ID NO:1 (2264) SEQ ID NO:2 (2285)	2289		2300		2310	é	2320	2330	2340
SEQ ID NO:1 (2264)	ATGC	TGAAAC	ATCATT	ACAGA	TTCTC	GCTAGC	CTGTTCTI	TTACC	ACTGACAG
SEQ ID NO:2 (2285)	ATGC	TGAAAC	ATCATT	ACAGA	TTCTC	GCTAGC	CTGTTCTI	TTACC	ACTGACAG
Consensus (2289)	ATGC	TGAAAC	ATCATT	ACAGA	TTCTC	GCTAGC	CTGTTCTI	TTACC	
									– Section 46
(2341)			50	236		2370		2380	2392
SEQ ID NO:1 (2316)	CTAG	ACACCT	AGAAAG	GAACT	GCAAJ	TATAA	CAAAACAA	GTACT	GGTTGACT
SEQ ID NO:2 (2337)									
Consensus (2341)	CTAG	ACACCT	AGAAAG	GAACT	GCAAI	TATAA	CAAAACAA	GTACT	
									- Section 47
(2393)	<u>2393</u>	2400		2410		2420	243	30	2444
SEQ ID NO:1 (2368)	TTCT	AATTAG	AGAGCA	TCTGC	AACAA	AAAGT	CATTTTTC	TGGAG	GGAAAAG
SEQ ID NO:2 (2389)	TTCT	AATTAG	AGAGCA	TCTGC	AACAZ	AAAGT	CATTTTTC	TGGAG	GGAAAAG
Consensus (2393)	TTCT	AATTAG	AGAGCA	TCTGC	AACAA	AAAGT	CATTTTTC	TGGAG	
									– Section 48
(2445)	2445	2450	2	460	2	470	2480		2496
SEQ ID NO:1 (2420)	CTTA	AAAAAA	TACTG	TGAAT	TGTTI	TTGTA	CAGTTATC	ATGAA	AAGCTTTT
SEQ ID NO:2 (2441)	CTTA	AAAAAA	TACTG	TGAAT	TGTTI	TTTGTA	CAGTTATC	ATGAA	AAGCTTTT
Consensus (2445)	CTTA	AAAAAA	TACTG	TGAAT	TGTTI	TTGTA	CAGTTATC	ATGAA	AAGCTTTT

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(	(2497)	2497			2510			2520		_	2530	) –		٠	Section	254
	(2472)	<u>~</u>	<u> </u>	<u>דידידי</u>	TNGC	CAAC	CAT	<u>ידנק</u> סמדי	C	TGT	<u>רבב</u>	<u>ה ה הי</u>	TCAC	ΔΩΤ	יעדעי	2.54 2.6(
seq ID no:1 ( seq ID no:2 (	(2493)	ጥጥጥጥ	ጥጥልጥ		TNGC	CAAC	CAT	TGC	CAA	TGT	~ א א ח	CAA	TCAC	AGT	ነ <u>ጸተ</u> ገ.	AG
Consensus (	(2497)	TTTT	TTAT	 TTTT:	INGC	CAAC	CAT	TGC	CAA	TGT	CAAT	CAA	TCAC	AGT	יאדעי	AG
															Section	
(	(2549)	2549		25	60		257	70		25	80		259	-		260
SEQ ID NO:1 (			GTTA			ACTG			CCA			тст				
SEQ ID NO:2 (																
Consensus (																
															Section	
(	2601)	2601		2610		2	620			2630			2640			2652
SEQ ID NO:1 (	2576)	TGCT	CAAA	GGTG	GCAA	GTTG	TCC	TGG	GTT	CTG	rgag	TCC	TGAG	ATG	GAT	TT7
SEQ ID NO:1 ( SEQ ID NO:2 (	2597)	TGCT	CAAA	GGTG	GCAA	GTTG	TCC	TGG	GTT	CTG	rgÅg	TCC	TGAG	ATG	GAT	TT?
Consensus (	2601)	TGCT	CAAA	GGTG	GCAA	GTTG	TCC	TGG	GTT	CTG	FGAG	TCC	TGAG	ATG	GAT	ΓTF
														<u> </u>	Section	ı 52
(	2653)	2653	26	60		2670	)		268	0		269	0			2704
SEQ ID NO:1 (	2628)	ATTC	TTGA	TGCT	GGTG	CTAG	AAG	TAG	GTC	TTC	AAAT	ATG	GGAT	TGT	TGT	ccc
SEQ ID NO:2 (	2649)	ATTC	TTGA	rgcto	GGTG	CTAG	AAG	TAG	GTC	TTC2	AAAT	ATG	GGAT	TGT	TGT	ccc
Consensus (	2653)	ATTC	TTGA	rgcto	GTG	CTAG	AAG	TAG	GTC	гтси	AAAT	ATG	GGAT	TGT	TGT	ccc
														<u> </u>	Section	ı 53
(	2705)	2705	2710		27	20		27	'30		2	740				2756
SEQ ID NO:1 () SEQ ID NO:2 ()	2680)	AACCO	CTGT	ACTGI	TOAS	CCCA	GTG	GCC	AAA	CTTZ	<b>ATTT</b>	ATG	CTGC	ТАА	ATG	AAA
SEQ ID NO:2 (	2701)	AACCO	CTGT	ACTGI	TOAS	CCCA	.GTG	GCC	AAA	CTT2	<b>ATTT</b>	ATG	CTGC	TAA	ATG	AAA
Consensus (2	2705)	AACCO	CTGT	ACTGI	ACT	CCCA	GTG	GCC	AAA	CTTZ	A T T T	ATG	CTGC	ΤΑΑ	ATG	AAA
	a	•												<u> </u>	Sectior	i 54
(2	2757)	2757			2770			2780			2790					2808
SEQ ID NO:1 ( SEQ ID NO:2 (	2732)	GAAA	GAAAA	AAAGO	AAA!	ΓΤΑΤ	ттт	TTT	TAT	CTT1	TTT	CTG	CTGT	GAC	GTT	C T A
SEQ ID NO:2 (	2753)	GAAAG	GAAAA	AAAGO	AAA'	FTAT	ΤΤΤ	TTT	TAT:	CTTJ	TTT	CTG	CTGT	GAC	GTT	[TA
Consensus (2	2757)	GAAAG	GAAAA	AAAGC	CAAA	TAT	ΤΤΤ	TTT	TAT:	ΓΤΤΊ	TTT	CTG	CTGT	GAC	GTT	ΓΤΑ
4 f		· • · · · ·		<u> </u>						· · ·					Section	
() 5EQ ID NO:1 ()	2809)	2809		28	20		_283	0		28	40		285	0		2860
5EQ ID NO:1 (2	2784)	GTCCC	CAGAC	TGAA	TTC	CAAA	TTT	GCT	CTAC	STTI	GGT	TAT	GGAA.	AAA	AGA	CTT
SEQ ID NO:2 (2	2805)	GTCCC	CAGAC	CTGAA	TTC	CAAA	ТТТ	GCT	CTAC	STTI	GGT	TAT	GGAA.	AAA	AGA	СТТ
Consensus (2	2809)	GTCCC	CAGAC	CTGAA	TTC	CAAA	ТТТ	GCT	CTAC	STTI	GGT	TAT	GGAA.			
														S	Section	56
	2861)			2870			880			890			2900			2912
SEQ ID NO:1 (2	2836)	TTTGC	CACI	GAAA	CTTC	GAGC	CAT	CTG	rgco	CTCI	AAG	AGG	CTGA	GAA	TGĠI	łAG
SEQ ID NO:2 (2																
Consensus (2	2861)	ጥጥጥሮሮ	ገሮአሮባ	מ ה ה יי	CTTTTC	- <u>&gt;</u> C C	~ <b>\ m</b>	$C \oplus C \oplus$	$\mathbf{r} \sim \sim$	תראיי	סגגי	3000	ግጥሮእ	~ ~ ~	TCCZ	1 D C

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								··		- Section 57
(291)	) <u>2913</u>	292	0	2930		2940		2950		296
SEQ ID NO:1 (288) SEQ ID NO:2 (290)	) AGT	TTCAGA	TAATAA	AGAGT	GAAGT	TTGCC	TGCA	AGTAAA	GAAT	TGAGAGT
SEQ ID NO:2 (290	) AGT	TTCAGA	TAATAA.	AGAGT	GAAGT	TTGCC	TGCAI	AGTAAA	GAAT	TGAGAGT
Consensus (291)	) AGT	TTCAGA	TAATAA	AGAGT	GAAGT	TTGCC	TGCA	AGTAAA	GAAT	
										- Section 58
(296	) <u>2965</u>	2970	······	2980		2990		3000		301
SEQ ID NO:1 (294)	) TGT	GCAAAG	CTTATT	TTCTT:	FTATC	TGGGC	AAAA	ATTAAA	ACAC	ATTCCTT
SEQ ID NO:2 (296										
Consensus (296	) TGT	GCAAAG	CTTATT	TTCTT	TATC	TGGGC	AAAA	ATTAAA	ACAC	ATTCCTT
										— Section 59
	) <u>3017</u>		,303		304		30			306
SEQ ID NO:1 (2992	) GAA	CAGAGC	TATTAC	TTGCC	rgttc	TGTGG	AGAA	ACTTTT	CTTT	TTGAGGG
SEQ ID NO:2 (3013	) GAA	CAGAGC	TATTAC	TTGCC	FGTTC	TGTGG	AGAA	ACTTTT	CTTT	TTGAGGG
Consensus (3017	) GAA	CAGAGC	TATTAC	TTGCC	IGTTC	TGTGG	AGAA	ACTTTT	CTTT	TTGAGGG
				*						- Section 60
(3069	) 3069		,3080		3090		3100		3110	312
5EQ ID NO:1 (3044	) TGT	GGTGAA	IGGATG.	AACGT	ACATC	GTAAA	ACTGA	CAAAA	TATT	TTAAAAA
SEQ ID NO:2 (3065										
Consensus (3069										
										Section 61
(3121	) 3121		3130	31	40	,31	50	3	160	317
SEQ ID NO:1 (3096	) ATA	ГААААС	ACAAAA'	TAAA	TAAA	GTTGC	TGGTC	CAGTCT	TAGTO	GTTTTAC
SEQ ID NO:2 (3117										
Consensus (3121										
						· · · · · · ·			·····	- Section 62
(3173	) 3173	,318	0	3190		3200		3210		322
SEQ ID NO:1 (3148					ACAG		TTGCI	CTGAG	TAAC	<b>IGACAAA</b>
SEQ ID NO:2 (3169										
Consensus (3173										
										- Section 63
(3225	) 3225	3230	-	3240		3250		3260		327
SEQ ID NO:1 (3200			TCAGT	TTTG	AGTA	AAGGC			AACA	AACAAAA
SEQ ID NO:2 (3221	CAG	AAACTA	TCAGT	TTTGI	AGTA	AAGGC	GTCAC	ATGCA	AACA	AACAAAA
Consensus (3225										
										- Section 64
(3277	) 3277		329	)	,330	0	,33	10		332
5EQ ID NO:1 (3252		TGAAAC							CACAZ	
SEQ ID NO:2 (3273										
	,									

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								Section 65
(3329)	3329	3	340	,3350	)	3360	3370	3380
SEQ ID NO:1 (3304)	TGAACT	GTGAA	GTGGT	TTAACAC	TGTATCC	TAGGCGAT	CTTTTT	TCCTCCT
SEQ ID NO:1 (3304) SEQ ID NO:2 (3325)	TGAACI	GTGAA	AGTGGT	TTAACAC	TGTATCC	TAGGCGAI	CTTTTT	TCCTCCT
Consensus (3329)	TGAACI	GTGAAA	GTGGT	ТТААСАС	TGTATCC	TAGGCGAI	CTTTTT	TCCTCCT
								Section 66
(3381)	3381	,3390	)	3400	341	0	3420	3432
SEQ ID NO:1 (3356) SEQ ID NO:2 (3377)	TCTGTT	TATTI	TTTGN	TTGTTTT	ATTTATA	GTCTGATI	TAAAAC	AATCAGA
SEQ ID NO:2 (3377)	TCTGTI	TATTI	TTTGN	TTGTTT	ATTTATA	GTCTGATI	TAAAAC	AATCAGA
Consensus (3381)	TCTGTT	TATTT	TTTGN	ITGTTT	ATTTATA	GTCTGATI	TAAAAC	AATCAGA
								Section 67
(3433)	3433	3440		3450	,3460	342	70	3484
SEQ ID NO:1 (3408)	TTCAAG	TTGGTI	AATTT	TAGTTAT	GTAACAA	CCTGACAI	GATGGA	GGAAAAC
SEQ ID NO:2 (3429)	TTCAAC	TTGGTI	AATTT	TAGTTAT	GTAACAA	CCTGACAT	GATGGA	GGAAAAC
Consensus (3433)								
								Section 68
(3485)	3485 3	490	350	0	3510	3520		3536
SEQ ID NO:1 (3460)	AACCTT	TAAAGO	GATTG	FGTCTAT	GGTTTGA	TTCACTTA	GAAATT	TTATTT
SEQ ID NO:2 (3481)								
Consensus (3485)	AACCTT	TAAAGG	GATTG	IGTCTAT	GGTTTGA	TTCACTTA	GAAATT	TTATTT
				,				Section 69
(3537)	3537		3550	3.	560	3575	5	
SEQ ID NO:1 (3512)	CTTATA	ACTTAA	GTGCA	ATAAAAT	GTGTTTT	TTCATGTT	,	
SEQ ID NO:2 (3533)	CTTATA	ACTTAA	GTGCA	АТААААТ	GTGTTTT	TTCATGTT	I	
Consensus (3537)	CTTATA	ACTTAA	GTGCA	ATAAAAT	GTGTTTT	TTCATGTT		

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